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OM of: US-09-155-327E-9 to: Issued_Patents_NA:* out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      About: Results were produced by the GenCore software, version 4.5\, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Date: Jun 6, 2002 2:32 PM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database sequences: 383533
Database length: 122816752
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Database: Issued_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MODEL_frame+_pin.model _DEV=xlh
-Q-/cgn2_1/(SPTO_spool)/US09155327/runat_06062002_084852_18504/app_query.fasta_1.508
-Q-/cgn2_1/(SPTO_spool)/US09155327/runat_06062002_084852_18504/app_query.fasta_1.508
-DB=Issued_patents_NA -QFMT=fastap -SUFFIX=pin.rni
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-COOPEXT=0.000 -GGAPEXT=0.000 -YGAPEXT=0.050 -YGAPEXT=0.000
-YGAPEXT=0.000 -GGAPEXT=7.000 -YGAPEXT=7.000 -YGAPEXT=0.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPEXT=5.000
-THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -DOCALIGN=200
-UTFMT-pfs -NORM-ext -HERPSIZE-500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09155327_eCGN1_1_118 -NCPU=6 -ICPU=3 -LONGLOG
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/Cgn2_6/ptodata/1/ina/5B_COMB.seq;US-08-978-523-1 + 1002.00 2101.54
/Cgn2_6/ptodata/1/ina/5B_COMB.seq;US-08-798-897-2 + 992.00 2080.38
/Cgn2_6/ptodata/1/ina/5B_COMB.seq;US-08-978-523-2 + 992.00 2080.38
/Cgn2_6/ptodata/1/ina/5B_COMB.seq;US-08-978-523-2 + 992.00 2080.38
/Cgn2_6/ptodata/1/ina/5B_COMB.seq;US-08-081-448-5 + 424.50 874.11
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1.50 874.11 5.3e-41 92
24.50 874.11 5.3e-41 9
424.50 874.11 5.3e-41
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/cgn2_6/ptodata/1/1na/PCTUS_COMB.seq:PCT-US94-07089-8 + 180
/cgn2_6/ptodata/1/1na/5A_COMB.seq:US-08-471-058-6 + 174.00
/cgn2_6/ptodata/1/1na/5B_COMB.seq:US-08-944-530-1 + 174.00
/cgn2_6/ptodata/1/1na/6A_COMB.seq:US-08-471-057-6 + 174.00
/cgn2_6/ptodata/1/1na/5A_COMB.seq:US-08-471-058-8 + 169.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-798-897-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-798-897-1
                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Applic Patent No. 5789201
                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 5.192
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-798-897-1 from: 1 to:
                                                                                                                                                                                                                                                                                                                        US-09-155-327E-9 x US-08-798-897-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Guaste
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Genes Codi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: by MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                  17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                               34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                       51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                         1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                    1 ATGGCGACCCCAGCCTCAACCCCCAGACACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                             eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
|||||||||||
                                            GGGAAGGCCCAGCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 1002.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Esmond, Robert W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KESSLER, GOLDSTEIN & FOX P.L.L.C.
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                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 98.964
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5.9e-11
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seq_documentation_block:
    Sequence 1, Application US/08978523
    Patent No. 5883229
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                      NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1433
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Guaste
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
ANDERSCENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501 GGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGGCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT 400
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                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 New
CITY: Washington
STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 GACGAGTTTGAGACCCGCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
                                                                                                               1483.0140002
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alignment_block:
US-09-155-327E-9 x US-08-978-523-1
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551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                    184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                           501 GCCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGGCCCTGG 550
                                                                                               167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                           451 TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                      151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                401 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA
                                                                                                                                                                                                                                                                        134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu
                                                                                                                                                                                                                                                                                                                                                           117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                  351
                                                                                                                                                                                                                                                                                                                                                                                                                     301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                         101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 GCTACACGTGACCCCAGGCTCAGCCCAGGCTTCACCCAGGTTTCCG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
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                                                                                                                                                                                                                                                                                                                                  ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT
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Ratio: 5.192
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                                                                                                                                                                                                                                                                                                                                     400
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Sequence 2, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:

APPLICANT:

Guastella, John

seq_documentation_block:

seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-798-897-2

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MOLECULE TYPE:
US-08-798-897-2
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US-09-155-327E-9 x US-08-798-897-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio: 5.167
Percent Similarity: 99.482
                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-798-897-2 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-3/1-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Genes Codi
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                   151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                             51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                          17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                          251 ATGAACTITTTCAAGGGGGGCCCCAACTGGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                      51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                     1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                         84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                     1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT 50
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1100 New York Avenue, N.W., Suite 600
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seq_documentation_block:
; Sequence 2, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
APPLICANT: Guastella, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-978-523-2
                                                                                    ; TOPOLOGY: bc
; MOLECULE TYPE:
US-08-978-523-2
                                         alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 TACGGGGACGGGCCTTGGAGGAGGCGCGCGTCTGCGGGAAGGGGAACTG 500
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                                                                                                                                                                                             TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/978,523
APPLICATION NUMBER: US/08/978,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 140
REFERENCE/TON INFORMATION:
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
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202-371-2540
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    Percent Identity: 97.927
                                                                                                                                                                                                                                                                    1483.0140002
                                         Length:
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alignment_block: US-09-155-327E-9 x US-08-978-523-2

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Sequence 5, Application US/08081448
Patent No. 5645008
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-081-448-5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-978-523-2 from: 1 to: 579
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STREET: 51.
STREET: 51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             501 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGGACTGGGGGCCCCTGG 550
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                                            COUNTRY: U
                                                                               ADDRESSEE: Arnold, White a purposition of the street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 424.50 Length: 224
Ratio: 2.989 Gaps: 4
Percent Similarity: 63.393 Percent Identity: 40.179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
500 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTC 549
                                                                                                                                450 AGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAG 499
                                                                                                                                                                                               400 CGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTC 449
                 95 rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
                                                                                      78 gPheThrGlnvalSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                                                                                                                                               350 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGCAAG 399
                                                                                                                                                              62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                                                                                                                              300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG 349
                                                                                                                                                                                                                                                                                                                                                                                             250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                 45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                              41 .....ProLeuHisGlnA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCCAG 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: NO. 5646008thrup, Thon REGISTRATION NUMBER: 33,268 REFERENCE/DOCKET NUMBER: ARCTELECOMMUNICATION INFORMATION: 312-744-0990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008thrun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOPTWARE: Patentin Release #1.0, Version #1.25
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312-755-4489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Balance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 199306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135..836
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128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145

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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-470-670A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08470670A
Patent No. 5834309
Patent No. 5834309 5710045
                              alignment_scores:
                                                                                     US-08-470-670A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 laGlupheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
                                                                                                                                                                                                                                            TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGACAGCCGAAAG 749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                           NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642 REFERENCE/DOCKET NUMBER: ARTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,448
                                                                                                                                        FEATURE:
                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                        LENGTH:
Quality:
Ratio:
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                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
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                                                                                                       CDS
135..836
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   424.50
2.989
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                      Length:
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alignment_block:
US-09-155-327E-9 x US-08-470-670A-6
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                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-481-739-1
                                                                                                                                                seq_documentation_block:
                                                                                                      Sequence 1, Application US/08481739 patent No. 6143291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 CGGGAGCTGGTTGACTTTCTCTCTACAAGCTTTCCCCAGAAAGGATA 199
                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 lametArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                                                                                 162 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
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APPLICANT: June, Carl H. and Thompson, Craig B.
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                             176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                       750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
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alignment_block:
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INFORMATION FOR SEQ ID NO: 1:
                                    397 AAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCA 446
                                                                                                           347 CAGCAGCAGTTTGGÀTGCCCGGGAGGTGATCCCCATGGCAGCAGTAAAGC 396
                                                                                                                                                                              300 TCCTGGCACCTGGCAGACAGCCCCGGGTGAATGGAGCC...ACTGGCCA 346
                                                                                                                                                                                                                                                     250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
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61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
                                                                      44 lnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThr 60
                                                                                                                                           35 uGlyProAlaAlaAsp.....ProLeuHisG 44
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TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/435,5
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. (GAD)
REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                .....ValCysGlyAlaGlyProGlyG1 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/481,739 FILING DATE: 07-JUNE-1995
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3.076
61.333
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alignment_block:
US-09-155-327E-9 x US-09-167-921-1
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APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
                                                                           Align seg 1/1 to: US-09-167-921-1 from: 1 to: 926
                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                     US-09-167-921-1
                                                                                                                                                                                                      Quality: 424.50
Ratio: 2.989
Percent Similarity: 63.393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                       FEATURE:

NAME/KEY: CDS

LOCATION: (135)..(836)

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: L20121 Genbank

DATABASE ENTRY DATE: 1994-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09167921A Patent No. 6172216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILE REFERENCE: ISPH-0324

CURRENT APPLICATION NUMBER: US/09/167,921A

CURRENT FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 926
TYPE: DNA
11 ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 rGlyAlaValAlaLeuGlyAlaLeu 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 ArgLeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuTh 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697 GGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGA 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 lAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597 GTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGC 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 ValAsnLysGluMetGluProLeuValGlyGlnValGlnAspTrpMetVa 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            497 GAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGG 546
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                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                              Percent Identity: 40.179
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seq_documentation_block:
    Sequence 39, Application US/09277020
    Patent No. 6210892
                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-277-020-39
                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Hennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
TITLE OF INVENTION: of mRNA Processing
FILE REFERENCE: ISPH-0339
FILE REFERENCE: ISPH-0339
                         SEQ ID NO 39
                                                                                                                CURRENT APPLICATION NUMBER: US/09/277,020 CURRENT FILING DATE: 1999-03-26 EARLIER APPLICATION NUMBER: 09/167,921
                                                                  EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAAGAACAGGACTGAGGCCCCAG 249
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                                                SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450 AGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAG 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AsnLysGluMetGluProLeuValGlyGlnValGlnAspTrpMetValAl 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
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LENGTH: 926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
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; ORGANISM: Homo sapiens US-09-277-020-39
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US-09-155-327E-9 x US-09-277-020-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 2.989
Percent Similarity: 63.393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-277-020-39 from: 1 to: 926
seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-323-743-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGGTAAACTGGGGTC 549
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                                                                                                                                                                                                                                               145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                         650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
                                                                                                                                                                                                                                                                                                                              128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
                                                                                                                                                                                                                                                                                                                                                                          600 GACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCAC 649
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                                                                                                                          750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG
                                                                                                                                                               162 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrG1 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 rgLeuValAlaphePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 gpheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                176 yAlaValAlaLeuGlyAlaLeu 183
                                           800 CGTGGTTCTGCTGGGCTCACTC 821
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seq_documentation_block:

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett p.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Alang, Oingoing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
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500 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTC 549
                                                                                      450 AGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAG 499
                                                                                                                                                                                400 CGCTGAGGGAGGCGACGAGTTTGAACTGCGGTACCGGCGGCATTC 449
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                        78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                   62 SeraspLeualaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                         45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAAGAACAGGACTGAGGCCCCAG 249
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2.989
63.393
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SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-461-511A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-461-511A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08461511A Patent No. 6303331 GENERAL INFORMATION:
                                                                                                                                                INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              800 CGTGGTTCTGCTGGGCTCACTC 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
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                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US/08/461,511A
FILING DATE: 05-Unn-1995
CLASSIFICATION: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: ARCD:179 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thompson, Craig B.B.
                                           NAME/KEY:
LOCATION:
                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                           TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                            IOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O. Box 4433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77210
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                                        135..836
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alignment_scores:

Quality: 424.50

Length:

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alignment_block:
US-09-155-327E-9 x US-08-461-511A-6
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; Sequence 6, Application PC/TUS9407089
; GENERAL INFORMATION:
                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US94-07089-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-461-511A-6 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              500 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTC 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600 GACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCAC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 AsnLysGluMetGluProLeuValGlyGlnValGlnAspTrpMetValAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           450 AGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAG 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400 CGCTGAGGGAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTC 449
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                        800 CGTGGTTCTGCTGGGCTCACTC 821
                                                                                                                                                                                                                                                                                                                                           176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 LeuArgGlu.....GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 .....ValCysGlyAlaGlyPro 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....ProLeuHisGlnA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG
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63.393
     Compositions and Methods
                                                           Vertebrate Apoptosis Gene:
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Percent Identity: 40.179
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alignment_block:
US-09-155-327E-9 x PCT-US94-07089-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22 JUNE 199
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/08:
FILING DATE: 22 JUNE 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 512-320-7200
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Appressee: Arnold, White & Durkee
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MOLECULE TYPE:
                                                                                                               347 CAGCAGCAGTTTGGATGCCCGGGAGGTGATCCCCATGGCAGCAGTAAAGC 396
                                                                                                                                                                                           300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCC...ACTGGCCA 346
                                                                                                                                                                                                                                                                       250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                                                                                                                                               200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLysGlyTy 27
                                                                                                                                                   35 uGlyProAlaAlaAsp......ProLeuHisG 44
                                                                                                                                                                                                                                                                                                                                                                                   61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
                                                                           44 lnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: PARKER, David L.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                         .....ValCysGlyAlaGlyProGlyGl 35
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Ratio:
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3.076
61.333
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5831066
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/08465485A
                TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
                                                                                                                FILING DATE: 22-DEC-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION UMBER: US 08/124,256
FILING DATE: 20-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497 GAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGG 546
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                                                                        NAME: Fortney, Andrew D. REGISTRATION NUMBER: 34,
                                                                                                                                                                                             APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/465,485A FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCT
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Y: U.S.A.
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1755 S. Jefferson Davis Hwy.,
(408) 436-2075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed, John
                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                      05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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                                                                                                                                                       us 07/288,692
                                                                          34,600
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                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
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alignment_block:
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    159 AlaArgArgLeuArgGluGlyAsnTrpAlaSerValArgThrValLeuTh 175
                                                                                                                                               528
                                                                                                                                                                               125 pMetValAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerG 142
                                                                                                                                                                                                                         478 GAGAGCGTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTG
                                                                                                                                                                                                                                                                                                         142 lyGlyTrpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGlu 158
                                                                                                                                                                                                                                                             109 GluSerValAsnLysGluMetGluProLeuValGlyGlnValGlnAspTr 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 GGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTGACGCCCTTCACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 TCCACCTGGCCCTCCGCCAAGCCGGCGACGACTTCTCCCGGCGCTACCGC
                                                                                                                                                                                                                                                                                                                                                                                      378 GCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGGGTGA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 TGCCCCGGCGCCGCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGG
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                                                                                                                                                                                                                                                                                                                                 92 snTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAla 108
                                                                                                                                                                                                                                                                                                                                                                                                                         75 aGlnGlnArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProA 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AspThrArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLy
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                           GATGACTGAGTACCTGAACCGGCACCTGCACCTGGATCCAGGATAACG
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Ratio:
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from:
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seq_documentation_block:
; Sequence 20, Application US/09080285
; Patent No. 6040181
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                                                     alignment_scores:
                                                                                                               US-09-080-285-20
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               TELEFAX: (408) 436-2075 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               666 TTTGGCCCTG...GTGGGAGCTTGCATCACCCTGGGTGCCTATCTGAGCC 712
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                  MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Arlington
STATE: Virginia
                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/080,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,600
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                                                                                                                                                                                                                                                           LENGTH:
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                 Quality:
Ratio:
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1755 S. Jefferson Davis Hwy., Suite 400
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1..717
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                                                                                                                                                                                                                                                                                                                                       (408) 436-2070
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22-DEC-1988
                                                                                                                                                                                      DNA (genomic)
 406.50
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   Percent Identity: 36.596
                                         Length:
                         Gaps:
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alignment_block:
US-09-155-327E-9 x US-09-080-285-20
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                                                                                                             seq_documentation_block:
                                                                                    ; Patent No. 5459251
                      ; SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 GCCGCATCCCGCGACCCGGTCGCCAGGACCTCGCCGCTGCAGACCCCGGC 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::||| |||:::||| |||||||||||:::|||::: |||:::|||
278 TCCACCTGGCCCTACGCCAAGCCGGCGACTTCTCCCGCCGCTACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 TGCCCCGGCGCCCCCGCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGG 277
                                            APPLICANT: TSujimoto, Yoshide; Croce, Carlo A. TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
                                                                                                                                                                                                                                                                                                                                              175 rGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaS 192
                                                                                                                                                                                                                                                                                                                                                                                                616 ATGCGGCCTCTGTTTGATTTCTCCTGGCTGTCTCTGAAGACTCTGCTCAG
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NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
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alignment_scores:
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                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,704
FILING DATE: 18-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 994,941
FILING DATE: 23-DEC-1992
APPLICATION NUMBER: 663,010
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: 883,687
FILING DATE: 09-JUL-1986
1986 GATGACTGAGTACCTGAACCGGCACCTGCACACCTGGATCCAGGATAACG 2035
                                                                                                                                                                                                                                                                                                                                                                   1836 GCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGCGGTGA 1885
                                                                                                                                                                                                                                                                                                                                                                                                                                        142 lyGlyTrpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGlu 158
                                                                                                        125 pMetValAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerG 142
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Ratio:
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Gaps: 5
Percent Identity: 36.596
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OM of: US-09-155-327E-9 to: EST:*
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Query: US-09-155-327E-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database sequences: 13736207
Database length: -1841457050
Search time (sec): 2329.970000
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-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
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-DELEXY=7.000 -START-1 -NANTRIX=blosum62 -TRANS=human40.cdi
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-NILEN=0 -MAXLEN=2000000000 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLENY -NANTT -THREADS=1
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gb_est2:BE293685
gb_est2:BE870269
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AL537680 AL537680 LTI_F1013_FB4
BG290422 602388270F1 NIH_MGC_93
BE647090 UI-M-BH1-alx-e-10-0-UI
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BW159253 TCBAPLE12081 Pediatrid
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7n88c09.x1 NCI_CGAP_OV
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S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Eukunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Kasukawa, T., Hayatsu, N., Hill, D., Hizamoto, K., Hiraoka, T., Hori, F., Hara, A., Hayatsu, N., Hill, D., Hizamoto, K., Hiraoka, T., Koda, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Quackenbush, J., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Salto, H., Saito, R., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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1949 bp mrNA linear HTC 19-JAN-Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930488D08:Bcl2-like 2, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes genome Res. 10 (10), 1617-1630 (2000)
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha
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BJ060637 BJ060637 NIBB MoChi
BF569393 6021855591 NIH_MGC
BE3778839 601237363F1 NIH_MGC
BE207063 ba09f05.y1 NIH_MGC_
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Tsurumi-ku, Yokohama

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alignment_block:
US-09-155-327E-9 x AK015644
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                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity: 100.000
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                                                         232 GGGAAGGCCCAGCCGCCGCTGCACCAAGCCATGCGGGCTGCTGGA 281
                                                                                                                                    182 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCTG 231
                                                                                                                                                                                                               132 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 181
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                           34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                          17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                    1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax:81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="matpastpdtralvadevgyklrokgyvcgagpgegpaadplho amraagdefetrerresdlaaolhvtpgsaooretovsdelpoggpnwgrlvaefvegaalcaesvnkemeplyggvodmwyayletrladwihssggwaeftalygdgaleear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAB29912.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  632 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       582 TACGGGGACGGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
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           Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikagami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                       Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P. and Hayashizaki,y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                             11042159
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (strain:C57BL/6J) adult male lung cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
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polyA_site
                                                   polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-2000) voshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) voshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Physical and Chemical Research Group, RIKEN Gemomic Sciences Center (GSC), Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                  /gene="BC1212"
209. .790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="MGD:MGI:1896837"
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3487
                                                                                                                                                                                                                                                                             putative'
                                                                                                                                                                                                                                                                                                                                    /note="Bcl2-like
                                                                                                                                                                                                                                                                                                                                                        /gene="Bc1212"
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                                                                                                                                                                                                                                                                                                             source key:MGI:108052, evidence:ISS
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AK004680 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 100.000
                                                                                         seq_documentation_block:
                                                                                                                                   seq_name: gb_est2:BE793530
                                                                        DEFINITION
SOURCE
               KEYWORDS
                            VERSION
                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 ATGGCGACCCCAGCCTCAACCCCAGACACGGGCTCTAGTGGCTGACTT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 GGGAAGGCCCAGCCGACCGACCCAAGCCATGCGGGCTGCTGGA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AspGluPhcGluThrArgPhcArgArgThrPhcScrAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                            134 euAlaAspTrpIleHiaSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                         559 TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                 659 TACGGGGACGGGCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 708
                                                                                                                                                                                                                                                                                                                          151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                       184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                             TGGCTGACTGGATCCACAGCAGTGGGGGGGTGGGCGGAGTTCACAGCTCTA 658
                                                                                                                                                                      TAACTGTAGGGGCCTTTTTTGCTAGCAAG 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 1006.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                 LUJU DP MRNA linear EST 20-SEP-2000 601590016F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5', mRNA securence
                               BE793530.1 GI:10214832
                                                               mRNA sequence.
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ORGANISM

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alignment_block:
US-09-155-327E-9 x BE793530
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AUTHORS
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JOURNAL
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                                                                                                  344 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 393
                                                                                                                                                                                                  294 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 343
                                                                                                                                                                                                                                                                                                  244 GGGAGGGCCCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA 293
                                                                                                                                                                                                                                                                                                                                                                                                  194 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 193
                                                                                                                             67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                          51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                          34 lyGluGlyProAlaAlaAspProLeuHiSGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                            17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
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High quality sequence start: 5
High quality sequence stop: 709.
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1 (bases 1 to 1030)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Organ: lung; Vector: poTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5/ adaptor: GGCAGGAG(6). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         945.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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alignment_scores:
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                                                                                                                              BASE COUNT
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      644 GCCATCAGTGAGGACAGTGCTGACGGGGGGGGGGTGGCACTGGGGGGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu. 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 694 GTAACTGTAGGGGCCTTT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 ValThrValGlyAlaPhe 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGGAGGGGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 eualaaspTrpIloHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 oLeuValGlyGlnValGlnAspTrpMetValA]aTyrLeuGluThrArgL 134
                      Quality:
                                                                                                                                                                                                                                                                                                                    No sl sequence available.
This clone (DKFZp761D0816) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1409 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg.Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                   German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S. EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Am Klopferspitz 18a D-82152 Martinsried, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Ansorge W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 804)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL157542.1 GI:7057943
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                                                                                                                            150 a
                                                                                                          /note-"Vector: pSport1; Site_1: Not1; Site_2: SalI"
217 c 294 g 142 t 1 others
943.00
4.911
                                                                                                                                                                                 /clone="DKF2p761D0816"
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/dev_stage="adult"
                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                .804
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Percent Similarity:

99.482

Percent Identity: 97.927

Ratio:

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alignment_block:
US-09-155-327E-9 x AL157542
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                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est2:BI770566
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                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                      KEYWORDS
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                                  COMMENT
                                                                                                            REFERENCE
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                                                                       TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 ATGAACTTTTTCAAGGGGCCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACGGGGACGGGCC.CTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                  603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5',
                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                   National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 697)
                                                                                                                                                                                                                             BI770566.1 GI:15762144
                                                                                                                                                                                                                                                                    mRNA sequence.
Email: cgapbs-remair.uiu.90v
Tissue Procurement: Life Technologies,
                                                                                          NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                               697 bp
                                                                                                                                                                                                                                                                                                                 mRNA
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alignment_block:
US-09-155-327E-9 x BI770566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA
                                              445 GTCTTTGGGGCTGCACTGTGTTGCTGAGAGTGTCAACAAGGAGATGGAAC 494
                                                                                                                                                             101 ValPheGlyAlaAlaLeuCys.AlaGluSerValAsnLySGluMetGluP 117
                                                                                                                                                                                                                               395 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                            51 AspGluPheGluThrArgPheArgArgThrPheScrAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lyGluGlyproAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
133 gLeualaaspTrpIleHisSerSerGlyGlyTrpalaGluPheThralaL 150
                                                                                                                                                                                                                                                             84 spGluLeupheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                       67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence start: 21
High quality sequence stop: 695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: LLAM11526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; /note="Organ: pool of 24 week female lung, 16 week female anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dready and directionally cloned (EcoRV site is destroyed primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size upon cloning in sommalized and enriched for range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:5209862"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NIH_MGC_122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
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percent Identity: 95.722
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_htc:AK013244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  645 CTGGGCACTCAGTGAGGACAGTTGCTGACGGGAGCCGTGGCACTGGGGGC 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 nTrpAla.SerValArgThrVal.LeuThrGlyAlaValAlaLeuGlyAl 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      595 TATACGGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGAGGGGAA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 euTyr.GlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAs 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409, 685-690 (2001)

5 (bases 1 to 854)
Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishil,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yoliake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muzamatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                           FANTOM Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AK013244 854 bp mRNA linear HTC 19-JAN-2002 Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810435A13:Bcl2-like 2, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK013244.1 GI:12850487
                                                                                                                                                                                                                                                                                                                                                                                                                     (sites)
RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (sites)
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                                              Quackenbush, J.,
                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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REFERENCE

MEDLINE TITLE JOURNAL

PUBMED

REFERENCE

AUTHORS

SOURCE KEYWORDS VERSION

ACCESSION

REFERENCE

JOURNAL

TITLE AUTHORS REFERENCE

PUBMED

TITLE JOURNAL

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MEDLINE JOURNAL TITLE AUTHORS

PUBMED

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Align seg 1/1 to: AK013244 from: 1 to: 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-155-327E-9 x AK013244
246 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                                                                                                               196 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 245
                                               17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                         1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper cDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with all subtraction to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Host: SOLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAGAGAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax:81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
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98.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="matpastpdfralvadfvgyklrokgyvcgagpgegpaadplho
amraagdefetrfrrtfsdlaaglhvtpgsagorftgvsdelfgggpnwgrlvaffvf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              data source:MGD, source key:MGI:108052, evidence:ISS
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196. .732
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/db_xref="GI:12850488"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Bc1212"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Second strand cDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 96.000
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346 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTGACCTGGCCGCTCA 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546 TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCTTTGGGGCTGCCCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         603069493F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 643)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                     High quality sequence stop: 643
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               Plate: LLAM11548 row: j column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                   http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
/note="Vector: pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV /note="Vector: pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV /note="Vector: pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of chon-activated adult donors. Library is oligo-dr primed non-activated adult donors. Library is reserved upon and directionally cloned (EcoRV site is destroyed upon and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range [1.2-3.3 kb, Library is normalized and enriched for full-length clones and was constructed by C. Gruber full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note:
                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:5218294"
/clone_lib="NIH_MGC_118"
                                                                                                                                                                 /tissue_type="leukocyte"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                    seq_name: gb_est2:BF785386
                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                     VERSION
                                 COMMENT
                                                                                                                REFERENCE
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                                                                                                                                                                         ORGANISM
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                                                                           TITLE
                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 evalGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCCCTTGTAGCCTTCTTT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 CACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 roLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGlu.MetGluP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                      587 CAAAGCTCGAGTCAGGGAGGATGGAGGAAGAAGCTGAGAAGCTAAAGGAG 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 uTyrGly......AspGlyAlaLeuGluGluAlaArgArgLeuArgGlu 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCTTTGGGGCTGCACTGTGTGTGCTGAGAGTGTCAACAAGGAGCATGGAAC 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                 602111728F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 815)
                                                                                                                                                                                                                      EST
                                                                                                                                                                                                                                       BF785386.1 GI:12090422
                                 Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 a
                                                                                                                                                                                                                                                                                 , mRNA sequence.
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184 c 216 g 114 t
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                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                           EST 12-JAN-2001
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seq_name: gb_est2:BI910270

seq_documentation_block:

DEFINITION

mRNA sequence.

ACCESSION

SOURCE KEYWORDS

ORGANISM

COMMENT

FEATURES

source

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REFERENCE

TITLE AUTHORS

JOURNAL

Unpublished (1999

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alignment_block:
US-09-155-327E-9 x BF785386
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397 GTGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCCTGGAG
                     141 erGlyGlyTrpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGlu 157
                                                                                                                124 pTrpMetValAlaTyrLeuGluThrArgLeuAlaAspTrpTleHisSers 141
                                                                                                                                                                              298 GCTGAGAGTGTCAACAAAGAAATGGAGCCTTG.GTGGGACAAGTGCAGGA 346
                                                                                                                                                                                                     108 AlaGluServalAsnLysGluMetGluProLeuValGlyGlnValGlnAs 124
                                                                                                                                                                                                                                                                    251 CTAACTGGGGCCGTCTTGTGGCATTCTTGTCTTGGGGC...TGCCTGTGT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                               91 roAsnTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCys 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 CGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTT.GAGACCCGTTTC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 ArgArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlySe 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 roLeuHisGlnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPhe 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 nLysGlyTyrValCysGlyAlaGlyProGlyGluGlyProAlaAlaAspp 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CCAGACACACGGGCTCTAGTGGTTGACTT.GTAGGCTATAAGCTGAGGCA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 ProAspThrArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGl 24
                                                                                        TTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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High quality sequence start: 3
High quality sequence stop: 650.
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Clone="IMAGE:4239798"
/Clone=lib="NCI_CGAP_Kid14"
/Clone=lib="NCI_CGAP_Kid14"
//lab_host="DH10B (T1 phage=resistant)"
/note="organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. | "
a 212 c 296 g 141 t
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96.774
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ORIGIN

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alignment_block:
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                                                                                                                                                                                                                                                                                                    Percent Similarity:
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17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                      99 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                 1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          495 GACGGGGGCCGTGGCACT.GGGGCCCCTGGTAACTGTAGGGGGCCCTTTTTGC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 TAGCACGT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 laserLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 uThrGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 GAGGCACGGGT.CTGCGGGAGGGGAACGG.GCATCAGTGAGGACAGTGCT 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GluAlaArgArgLeuArgGluGlyAsnTrpAlaSerValArgThrValLe 174
                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAN10394 row: e column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 792)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BG298789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511215 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG298789.1 GI:13063794
                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 a
                                                                                                                                                                                                                                                                                                                                                                                                                                  //db_xref="taxon:10090"
//db_xref="taxon:10090"
/clone="IMAGE:4511215"
/clone="IMAGE:4511215"
/clone="IMAGE:4511215"
/clone="Ibl="NIH_MGC_94"
/fissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                               739.00
5.097
99.315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                          Percent Identity: 98.630
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seq_name: gb_est1:AW258810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 GACGAGITIGAGACCCGITICCGCCGCACCITCTCTGACCTGGC.GCTCA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 valPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGAAGGCCCACCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 540)

1 (bases 1 to 540)

1 (bases 1 to 540)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person Underwood, K., Steptoe, M., Pape, D., Harvey, N., Schurk, R., Ritter, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Waterston, R. and Wilson, R. Waterston, R. and Wilson, R. and R. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        um74a02.yl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:2300906 5' similar to SW:BCLW_MOUSE P70345 APOPTOSIS
REGULATOR BCL-W. [2] SW:BCLW_MOUSE ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW258810.1 GI:6631791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nouse mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:1009678
                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouseest@watson.wustl.edu
                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:2300906"
/clone_lib="Sugano mouse kidney mkia"
                                                                                                                                                                                                                                                         /organism="Mus musculus"
/lab_host="DH10B"
                                                                      /sex="female"
                                                                                                                                                                                                                      /strain="C57BL"
                           /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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SOURCE
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alignment_scores:
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                                                                                    seq_name: gb_est2:BI764428
                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 ATGGCGACCCCAGCCTCAACCCCAGACACACGGCCTCTAGTGGCTGACTT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                          412 GTCTATGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                                                                                                                    101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                              462 TTTGGTGGGACAAGTGCATGATTGGATGGTGGCCTACCTGGAGACACGTC
                                                                                                                                                                                                                                                                          117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
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                                                                                                                                    512 TGGCTGACTGGATCACAGCAGTGGGG 537
                                                                                                                                                                                 134 euAlaAspTrpIleHisSerSerGly 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetalaThrproAlaSerThrproAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
603050701F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190792 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was [ATGTGGCCTTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was lighted to a Draili adaptor [TGTTGGCCTACTGG], digested lighted to a Draili sites of the pME18S-FL3 and cloned into distinct Draili sites of the pME18S-FL3 and cloned into distinct Draili sites cACCATGTG). XhoI should vector (5' site CACTGTGTG, 3' site CACCATGTG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: kidney; vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
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5.150
98.592
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                                          mRNA
                                            linear
                                               EST 25-SEP-2001
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BI764428.1 GI:15756006

mRNA sequence

human.

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 576.00
Ratio: 5.143
Percent Similarity: 100.000
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389 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 438
                                                                                                              339 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 388
                                                                                                                                                                                                                                289 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 338
                                                                                                                                                                                                                                                                                                                                              239 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCCG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 188
                           84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                             34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAlaThrFroAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                     nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov plate: LLAM11477 row: a column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 758)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="0rgan: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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/clone="IMAGE:5190792"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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alignment_block:
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AUTHORS
                                                                                                                                                                                                                                                                                Align seg 1/1 to: BM191403 from: 1 to: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                               US-09-155-327E-9 x BM191403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                          169 TGTT.....CCAGAGCCTGCAGGACCAGCATCCTGTGCTTTGCATT 209
                                                                                                                                                                                   119 CGGGCTTTGGTGGAGGATTTTGTGCGGTACAAGTTATGCCAACGTAGTCT 168
210 CAGCTATGCGTGCTGCAGGGGATGAATTTGAGGAGCGATTCAGACAAGCA 259
                        27 rValCysGlyAlaGlyProGlyGluGlyProAlaAlaAspProLeuHisG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsn 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 GTCTTTGGGGCTGCACTGTGTGCTGAAAGTGTTTCC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov High quality sequence stop: 386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 African clawed frog.
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM191403
601 bp mRNA linear EST 11-DEC-2001 daj86a10.yl NICHD XGC Lil Xenopus laevis cDNA clone IMAGE:5129754
5' similar to SW:AR1_XENLA Q91827 APOPTOSIS REGULATOR R1 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM191403.1 GI:17527366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases I to 601
                                                                                                                                                                                                                                                                                                                                                                                                      572.50
4.119
84.756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC)) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:5129754"
/clone_lib="NICHD XGC Lil"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xenopus laevis"
/db_xref="taxon:8355"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 g
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LOCUS AA596919 362 bp mRNA linear EST 19-SEP-199
DEFINITION vo21f08.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
IMAGE:1050567 5' similar to TR:E123735 E123735 R1 MRNA. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 GTCAACAAGGAGATGTCCCCCTCTTCTGCCACGGATTCAAGACTGGATGGT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 GGCGTATAGTTGCATTTTTTGTTTTTGGTGCCGCACTGTGTGCTGAGAGT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510 GGAATGGATTTCTAACTCTATATGGGGATGGTGCCATAGAAGAAGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 rpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 lalaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 ValAsnLysGluMetGluProLeuValGlyGlnValGlnAspTrpMetVa 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PheSerAspLeuAlaAlaGinLeuHisValThrProGlySerAlaGinGl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 lyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSer 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 nArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpG 94
                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACATATCTGGAGACAAACCTGAGAGGCTGGATTCAGAGCAATGGAGGCT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 362)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA596919.1 GI:2412354
                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                          High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                         primer: -28m13 rev2 ET from Amersham
/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cI
                                                                     /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
                                                                                                                         /clone="IMAGE:1050567"
                                                                                                                                                                       /strain="C3H"
                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                              /db_xref="taxon:10090"
                                              /lab_host="DH10B"
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                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                   REFERENCE
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                                                                                                                                                                       TITLE
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alignment_scores:
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US-09-155-327E-9 x AA596919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est2:BF204905
                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                          AUTHORS
                                                                                                              JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 CGTGACCCCAGCCTCAGCCCAGCAACGCTTCACCCAGGTTTCCGACGAAC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 TTTGAGACCCGTTTCCGCCGCACCTTCTCTGAACTGGCCGCTCAGCTACA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 GlyAlaAlaLeuCysAlaGluSerValAsnLys 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 TTTTCCAAGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 CTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 yTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProGlyGluG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPheValG1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 PheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGlnLeuHi 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 lyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGlyAspGlu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 sValThrProGlySerAlaGlnGlnArgPheThrGlnValSerAspGluL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 euPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePheValPhe 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCTGCCCTGTGTGCTGAGAGTGTCACAAAG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                       601866718F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106836 5',
                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                          BF204905.1 GI:11098491
                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                     (bases 1 to 601)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            characteristic muscle proteins a 116 c 107 g 75 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3/]; double-stranded cDNA was ligated to Eco RI adaptors [AATTCCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rapidly, forming contractile myotubes and producing
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                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 06-NOV-2000
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seq_name: gb_est2:BE508939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-155-327E-9 x BF204905
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                                                                                                                                                                                                                 118 LeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgLe 134
                                                                                                        134 uAlaAsp.TrpIleHisSerSerGlyGly 143
                                                                                                                                                                                                                                                                                 465 TCTTGGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGGAGATGGAACCA 514
                                                                                                                                                                                                                                                                                                                101 alPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPro 117
                                                                                                                                                                                                                                                                                                                                                                                                415 GAACTGTTTGCAAGGGGGCCCCAACTGGGGTTCGCTTGTAGCCCTTCTTGG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 TCATGTGATCCCAGGCTCAGCCCAACAACGACTTCACCCAGGTCTCCGAT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 GTTCGAGACCCCCTTCCGGCGTCACCTTCTCTGATCTGGCGGCTCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 GGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGAGATGA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 GTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 .HisValThrProGlySerAlaGlnGlnArg.PheThrGlnValSerAsp 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 CCAGCCTCGGCCCCAGACCACAACCGGGCTCTGGTGGCAGACATTTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                  85 GluLeuPhe.GlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePheV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 uPheGluThrArgPheArgArg.ThrPheSerAspLeuAlaAlaGlnLeu 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 GlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGlyAspGl 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 lyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProGlyGlu 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ProAlaSerThrProAsp...ThrArgAlaLeuValAlaAsp.PheValG 19
                                                       GGCTGATCTGGATCCAAAGAGAGTGGGGT 593
                                                                                                                                                                   CTGGTGGGACAAGTGCAGGAGTGGATGGTGGCTACTGTGAGACGCGGTCT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.lln1.gov
plate: LLCM987 row: d column: 05
High quality sequence stop: 561.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="rhabdomyosarcoma"
/lab_host="DHIUB (phage resistant)"
/note="organ: muscle; Vector: pOTB7; Site_1: ECORI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Site-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 176 c 201 g 114 t
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4.199
90.476
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/clone="IMAGE:4106836"
/clone_lib="NIH_MGC_17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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alignment_block:
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: BE508939 from: 1 to: 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
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312 ACGATTTGCTGAAGTAGCAGGTAGCCTGTTCCAAGGAGGGGTGAATTNGG 361
                                                                                                         262 TTCAGTGAGATCTCCACACAGATCCACGTGACCCCGGCACAGCATATGC 311
                                                                                                                                                                                                                  212 CAGCTATGCGTGCTGCAGGGGATGAATTTGAGGAGCGATTCAGACAAGCA 261
                                                                                                                                                                                                                                                                                                                           171 TGTT.....CCAGAGCCTGCAGGACCAGCATCCTGTGCTTTGCATT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CGGGCTTTGGTGGAGGATTTTGTGCGGTACAAGTTATGCCAACGTAGTCT 170
                          77 nArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpG 94
                                                                                                                                                          61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
                                                                                                                                                                                                                                               44 lnAlametArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThr 60 ::||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                27 rValCysGlyAlaGlyProGlyGluGlyProAlaAlaAspProLeuHisG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLysGlyTy 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov Seq.primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE508939 612 bp mRNA linear EST 07-AUG-2000 dc14h09.yl NICHD XGC Lil Xenopus laevis cDNA clone IMAGE:3397121 5' similar to SW:AR1_XENLA Q91827 APOPTOSIS REGULATOR R1 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 African clawed frog.
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE508939.1 GI:9728714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
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1 128 c 188 g 141 t 1 others
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/lab_host="PHIOB (phage-resistant)"
/not="Organ: liver; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.928
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SIDS1/gegdata/geneseq/geneseqn-embl/NA199 DAT:AAX2833 + 1002.00 1897.54 2.46
SIDS1/gegdata/geneseq/geneseqn-embl/NA199 DAT:AAX2833 + 1002.00 1897.54 2.66
SIDS1/gegdata/geneseq/geneseqn-embl/NA199 DAT:AAX2833 + 992.00 1878.49 2.86
SIDS1/gegdata/geneseq/geneseqn-embl/NA199 DAT:AAX2833 + 992.00 1878.49 2.86
SIDS1/gegdata/geneseq/geneseqn-embl/NA199 DAT:AAX2833 + 992.00 1874.61 4.56
SIDS1/gegdata/geneseq/geneseqn-embl/NA199 DAT:AAX2833 + 428.00 799.65 3.44
SIDS1/gegdata/geneseq/geneseqn-embl/NA2001 DAT:AAX2833 + 428.00 799.65 3.44
SIDS1/gegdata/geneseq/geneseqn-embl/NA2001 DAT:AAX2833 + 428.50 792.70 8.3
SIDS1/gegdata/geneseq/geneseqn-embl/NA2001 DAT:AAX1936 + 428.50 792.70 8.3
SIDS1/gegdata/geneseq/geneseqn-embl/NA2001 DAT:AAX3189 + 428.50 772.35 1.44
SIDS1/gegdata/geneseq/geneseqn-embl/NA2001 DAT:AAX3189 + 428.50 772.35 1.44
SIDS1/gegdata/geneseq/geneseqn-embl/NA2001 DAT:AAX3180 + 406.50 760.32 4.55
SIDS1/gegdata/geneseq/geneseqn-embl/NA2001 DAT:AAX3180 + 406.50 781.32 5.3
SIDS1/gegdata/genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      About: Results were produced by the GenCore software, version 4.5 Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -0-/cgn2_1/USPTO_spool/US09155327/runat_06062002_084853_18524/app_query.fasta_1.508
-DB-N_Geneseq_032802 -OPMT=fastap -SUFFIX=p2n.rng -GAPOP-12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPEXT=0.000 -GAPEXY=0.050 -XAPOP=10.000 -XAPEXT=0.500
-FGAPOP=4.500 -OGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELEXT=7.000 -START=1 -MATRIX=blosum62
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -TR_SCORE=PCt
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -TR_SCORE=Pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pfs
-NORM=0xt -HEAPSITE=500 -NINLEN=0 -MAXLEN=200000000
-NORM=0xt -HEAPSITE=500 -NINLEN=0 -MAXLEN=200000000
-NORM=0xt -HEAPSITE=500 -NINLEN=0 -MAXLEN=2000000000
-USER=US09155327_@CGN1_1_0 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search time (sec): 288.150000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database sequences: 1736430
Database length: 858457221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query length: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query:
                                                                                            /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX33184 +
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH45296 +
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:AAQ54631 +
/SIDS1/gcqdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH45297 + /SIDS1/gcqdata/geneseq/geneseqn-emb1/NA2002.DAT:ABL32229 - /SIDS1/gcqdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF30926 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-155-327E-9
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772.35
760.92
                                                              753.30
729.16
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3.4e-36
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4 5.3e-34
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1.1e-32
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4.9e-34
4.9e-34
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1.5e-35
5.8e-36
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alignment_scores:

Quality: 1006.00 Ratio: 5.212 Percent Similarity: 100.000

Opercent Identity: 99.482

Length:

alignment_block:

US-09-155-327E-9 x AAX25133 Align seg 1/1 to: AAX25133

1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17

from: 1 to: 581

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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAH48169 + 400.06
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:AAT33694 + 396.50
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:AAQ81696 + 383.00
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:AAV17638 + 371.50
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:ABA73433 - 369.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID      AAX25133 standard; DNA; 581 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX25133
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    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-1999 (first entry)
                                                                                                                                                                                                                      The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see AAY05531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                animal model; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse bcl-w gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9913710-A1.
                                                       for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bol-w gene or in a gene associated with bol-w. Such animal have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in inducing, enhancing or otherwise facilitating spermatogenesis in
                                                                                                                                                                                                                                                                                                                                                                                                                                  An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY05531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 34; 52pp; English
Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;
                                          animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cory S, Gibson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97AU-0009228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-AU00764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koentgen F, Print C;
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710.45
687.71
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3.2e-31
5.9e-30
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seq_documentation_block:
ID AAV28333 standard; cD
XX

AC AAV28333;
XY

DT 02-OCT-1998 (first e
XX

DE Rat bcl-y gene.
XX

KW 8s; bcl-y; bcl-2; cel
XX

KW 8s; bcl-y; bcl-2; cel
XX

FH Key
FT CDS
FT C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV28333 standard; cDNA; 579 Bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 eualaaspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 GCTACACGTGACCCCAGGCTCAGCCCAGCCTTCACCCAGGTTTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProg 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGGCCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspGluPheGluThrargPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0798897
                                                                                                                                                                                                                                                                                 /product= bcl-y
                                                                                                                                                                                                                                                                                                                               /*taq=
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                              "No stop codon given"
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alignment_block;
US-09-155-327E-9 x AAV28333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAV28333 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity: 100.000
134 eualaaspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu
                                                             351 ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT
                                                                                               117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                           301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                              101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                       251 ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTF 300
                                                                                                                                                                                                                                                                                                   151 GACGAGTTTGAGACCCGCCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 GGGAAGGCCCAGCCGACCGGCTGCACCAAGCCATGCGGGCAGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.
                                                                                                                                                                                                                                          84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                      51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Column 13/14; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAW61391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-446079/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetalaThrProalaSerThrProAspThrArgAlaLeuValalaAspPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                         \verb|nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 1002.00
Ratio: 5.192
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97US-0798897.
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Gaps:
                         150
                                                                                                                                                                                                                                                                                                       250
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAX15945
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The present sequence encodes rat bcl-y protein (Rbcl-y). The cy specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC proteins may be used to treat conditions associated with a disruption of CC proteins may be used to treat conditions associated with a disruption of CC conditions associated with a disruption of CC calleimer's Disease, neural and muscular degenerative diseases and treat subjects suffering from: strokes, head trauma, CC cell death, aging, spinal cord injuries and amyotrophic lateral cCC cell death, aging, spinal cord injuries and amyotrophic lateral as a cclerosis conditions where cells under go premature cell death as a cclerosis conditions where cells under go premature cell death as a cclerosis way to develop cell lines which remain viable in culture for cused in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, cc Rbcl-y and Hbcl-y may be used to treat conditions associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; nultiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 GGCATCAGTGAGGACAGTGCTGACGGGGGCCTGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX15945 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA encoding the rat bcl-y protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parasite; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Columns 13-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel bcl-y homologues of the rat and human bcl-2 protein \, - useful for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-214150/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
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97US-0798897.
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seq_documentation_block:
ID AAX25132 standard; DNA; 581 BP

05-JUL-1999 (first entry)

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SSSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAX15945 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-155-327E-9 x AAX15945
seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX25132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 GACGAGTTTGAGACCCGCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
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                                                                                                                                                                                                                                                                                                                              134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGlupheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                              117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                        351 ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                                                                                                                         451 TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                          551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                               167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCGACCCCAGCCTCAACCCCAGACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGAAGGCCCAGCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                               TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                           GGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGCCCCTGG
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Ratio: 5.192
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Percent Identity: 98.964
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                          US-09-155-327E-9 x AAX25132
                                                                                                                                                                                                                                                                                                                                                                                              Quality: 997.00
Ratio: 5.166
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the human bcl-w gene encoding Bcl-w protein C (see AAY05530), a pro-survival member of the Bcl-2 family which is carefully expressed and which is essential for spermatogenesis. The C invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic Sequences useful for inducing or reducing fertility of male C animals. Methods are provided for the treatment of infertility, or C model carries a mutation is at least one allele of the human or C model carries a mutation is at least one allele of the human or C marine bcl-w gene or in a gene associated with bcl-w. Such animals C infertile, but possess no other major abnormalities as determined C by histological examination. They can be used to screen for C inducing, enhancing or otherwise facilitating spermatogenesis in animals. Or which can indice infertilety.
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                                                                       101 GGGAGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other;
                                                                                          34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                              51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                  17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 32; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                                      1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 50
                                                                                                                                                                                                                                       1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-243890/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         animal model; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bcl-w gene
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                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 98.446
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seq_documentation_block:
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growth e.g. cancers
  Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                    WPI; 1998-446079/38
                                                                                                 Guastella J;
                                                         P-PSDB; AAW61392
                                                                                                                                                                    23-FEB-1996;
                                                                                                                         (COCE-) COCENSYS INC
                                                                                                                                                        11-FEB-1997;
                                                                                                                                                                                                11-FEB-1997;
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                                                                                                                                                                                                                                                       US5789201-A.
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                   ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV28334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV28334 standard; cDNA; 579 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 GCCATCAGTGACGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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                                                                                                                                                     96US-0012201.
97US-0798897.
                                                                                                                                                                                               97US-0798897
                                                                                                                                                                                                                                                                         /product= bcl-y
/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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alignment_block:
US-09-155-327E-9 x AAV28334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAV28334 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression in vivo. Also, antisense const where prevention of cell death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    falls in the apoptosis activity category. The recombinant protein may falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders expression in vivo. Also, antisense constructs can be used in disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Column 15/16; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                      351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                 401
                                                                                                                                                                                                                                                                                                            134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGAGITCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                            TGGCTGACTGGATCCACAGCAGTGGGGGGGCTGGGGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                      ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                            oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                       euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                          pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                            TACGGGGACGGGGCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG
TAACTGTAGGGGCCTTTTTTGCTAGCAAG
                                          alThrValGlyAlaPhePheAlaSerLys 193
                                                                                       GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     992.00
5.167
99.482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 97.927
       579
                                                                                                                                                                                                                                                                                                                                                                       400
                                                                                                                                                                                                                                                                                                                                                                                                                                                            350
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alignment_block:

Percent Similarity:

US-09-155-327E-9 x AAX15946

alignment_scores:

Quality: Ratio:

992.00 99.482

Percent Identity: 97.927 Length: Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX15946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
CC specification also describes rat bolly protein (Rboll-y). Rboll-y and CC specification also describes rat bolly protein (Rboll-y). Rboll-y and CC specification also describes rat bolly protein thought to be involved in CC programmed cell death (apoptosis and necrosis). Rboll-y and Hbolly CC proteins may be used to treat conditions associated with a disruption of CC proteins may be used to treat subjects suffering from: strokes, they may be CC used in therapies to treat subjects suffering from: strokes, they may be CC (especially multiple sclerosis), myocardial infarction, vitally induced CC (especially multiple sclerosis), myocardial infarction, vitally induced CC (especially multiple sclerosis), myocardial infarction, vitally induced CC cell death, aging, spinal cord injuries and amyotrophic lateral CC sclerosis conditions where cells under go premature cell death as a CC sclerosis conditions where cells under go premature cell death as a CC used in this way to develop cell lines which remain viable in culture for CC used in this way to develop cell lines which remain viable in culture for CC an extended period. In contrast, if they act as cell death stimulators, Rboll-y and Hboll-y may be used to treat conditions associated with CC considered with the conditions associated wit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Raposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX15946 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding the human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5883229-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parasite; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Columns 15-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel bcl-y homologues of the rat and human bcl-2 protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes human bcl-y protein (Hbcl-y).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW97392
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97US-0978523.
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seq_documentation_block:
ID AAT96577 standard; DNA; 583 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AAT96577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAX15946 from: 1 to: 579
W09735971-A1
                                                                                                                                                                                                                 Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                         diagnosis; degenerative disease; ss
                                                                                                                                                                                                                                                                                    Human bcl-w DNA.
                                                                                                                                                                                                                                                                                                                         22-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGGCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 GGGAGGGCCCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 ASPGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACGGGGACGGGCCCTGGAGGAGGCGCGCGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCTGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheFhrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCTTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT 50
                                          /product= bcl-w
                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250
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alignment_block:
US-09-155-327E-9 x AAT96577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 100.000
                 101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                            251 ACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                             201 GCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                             151 GATGAGTTCGAGACCCGCCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
                                                                                                                                                                                                                                                                                                                              101 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGCCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
                                                                                                    84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                     67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
                                                                                                                                                                                                                                                                     51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                             51 TGTAGGTTÄTAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                  17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 48; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams JM, Cory S, Gibson LM, Holmgreen SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW36047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-489635/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMRA-) AMRAD OPERATIONS PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96AU-0008965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-AU00199
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5.130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 97,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                               200
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351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                         167
                                                                                                                                             451
                                                                                                                                                                             151
                                                                                                                                                                                                                 401
551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                             TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                        pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                     oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                   alThrValGlyAlaPhePheAlaSerLys 193
                                                                     GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                           TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG
                                                                                550
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX25134

seq_documentation_block:

AAX25134 standard; DNA; 583 BP.

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Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility; animal model; ss.
                                                                                                                                                                               W09913710-A1
                                                                                                                                                                                                                          05-JUL-1999 (first entry)
                                                                                                                                                                                                                                   AAX25134;
                                                                                                                                                 16-SEP-1997;
                                                                                                                                                           16-SEP-1998;
                                                                                                                                                                                        Homo sapiens
                                                                                                                             Adams J, Cory S, Gibson L,
                                                                                                                                      (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                     25-MAR-1999
                                                                                                                                                                                                               bc1-w gene derivative
                                                                                                                                                  97AU-0009228.
                                                                                                                                                            98WO-AU00764.
                                                                                                                                Koentgen F,
                                                                                                                                Print C;
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P-PSDB; AAY05532. WPI; 1999-243890/20.

An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w $\,$

Disclosure; Page 36; 52pp; English.

The present sequence is described as a derivative of the human bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries

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SSX
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                                                                                                                                                                 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AAT96578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAX25134 from: 1 to: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-155-327E-9 \times AAX25134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 100.000
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 583 BP; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 CTCTTTGGGGCTGCACTGTGTGTGTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 ACGAACTITTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 GCTGCATGTGACCCCAGGCTCAGCCAGCAACGCTTCACCCAGGTCTCCG
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                                                                                                                                                                                                                                                                                       167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                             134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
              Mouse bcl-w DNA.
                                                                                                                                                                                                       551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG
                                                                                                                                                                                                                                      184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                           501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-1998
                                                                                                                 AAT96578 standard; DNA; 581 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                         GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                             TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                             TGGTCGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA
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                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.409
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alignment_scores:
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                                                                                                                                                                                                                                                                                                           US-09-155-327E-9 x AAT96578
                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
151 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's diseases, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w modilitates; antibody production or screening of potential
                                                                          101
                 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                  34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                  51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 581 BP; 105 A; 164 C; 195
                                                                                                                                                     17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 50-51; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW36048
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                                                                                                                                                                                                    1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
diagnosis; degenerative disease; ss.
                                                                                                                                                                                                                     1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                   GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96AU-0008965
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98.446
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/note= "q"
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                                                                                                                                                                                                                                                                                                                                           vaps: 0
Percent Identity: 96.373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                         193
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX25135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                 An animal model exhibiting reduced levels protein associated with Bcl-w
                                                                                          P-PSDB; AAY05533
                                                                                                                                                                                                                                                                                                      CDS
                                                                                                     WPI; 1999-243890/20.
                                                                                                                                                    (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                   16-SEP-1997;
                                                                                                                                                                                                          16-SEP-1998;
                                                                                                                                                                                                                                     25-MAR-1999.
                                                                                                                                                                                                                                                              W09913710-A1
                                                                                                                                                                                                                                                                                                                                           Mus sp.
                                                                                                                                                                                                                                                                                                                                                                      animal model;
                                                                                                                                                                                                                                                                                                                                                                           Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                       Mouse bcl-w gene derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX25135 standard; DNA; 581 BP
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                                                                                                                            Cory S, Gibson L,
                                                                                                                                                                                97AU-0009228.
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                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                            Koentgen F,
                                                           of
                                                           a Bcl-w protein and/or
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The present sequence is described as a derivative of the mouse

Disclosure; Page 38;

52pp; English.

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAX25135 from: 1 to: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -09-155-327E-9 x AAX25135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including generic sequences capable of inducing, enhancing or otherwise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          facilitating spermatogenesis in animals, or which can induce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ValpheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTG 100
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                                                                                                                                                                                                                                     401
                                                                                                                                                                                                                                                                                              134
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                            167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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TACGGGGACGGGCCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTG 500
                                                                                                                                                                      TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                     TGGCTGACTGGATCCACAGCAGTGGCGGCTGGGCGGACTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                      TTTGGTGGGACAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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98.446
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ID AAV41925 standard; cDNA; 1098 BP
                                                                                                                                                                                        alignment_scores:
                                                                        alignment_block:
                                                                                                     Percent Similarity: 100.000
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                                                         US-09-155-327E-9 \times AAV41925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 alThrvalGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bc1-like (HAICH29); chronic inflammatory disease; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunological disorder; autoimmune disease; anti-infectious agent;
                                                                                                                                                                                                                 This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-1997;
21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9831800-A2.
                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-1998.
                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                      or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-414099/35.
P-PSDB; AAW59884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feng P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AUCK-) AUCKLAND UNISERVICES LTD
                                                                                                                                                                                        Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gentz RL, Krissansen GW,
                                                                                                                     Ratio:
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97US-0034204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Bcl-like (HAICH29) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                     756.00
                                                                                                                       5.250
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                                  from: 1 to: 1098
                                                                                                        Percent Identity: 97.917
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                                                                                                                                      Length:
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/Na1998.DAT:AAV59630
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07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                   Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; inmune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                  06-MAR-1998;
                                                                                                                                                                                                                                  11-SEP-1998
                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                   WO9839448-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein gene 120 clone HGBGZ64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV59630 standard; DNA; 1864 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspGluPheGluThrargPheArgArgThrPheSorAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGCTGACTGGATCCACAGCAGTGGGGGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                                                                                                                                                                                                 sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
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97US-0038621
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                                                                                                                                                                                               98WO-US04493
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23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
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23-MAY-1997;
23-MAY-1997;
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97US-0048971.

97US-0049510.

97US-00551926.

97US-0055724.

97US-0056630.

97US-0056631.

97US-0056632.

97US-0056635.

97US-0056636.

97US-0056636.
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97US-0047615.
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97US-0047633.
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97US-0047612.
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97US-0043313.
97US-0043314.
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alignment_block:
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                                                                                                                                                                                                                     Align seg 1/1 to: AAV59630 from: 1 to: 1864
                                                                                                                                                                                                                                                        US-09-155-327E-9 x AAV59630
                                                                                                                                                                                                                                                                                                               Percent Similarity: 100.000
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22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feng P,
Kyaw H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCC 209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic rate invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAV74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in polypucleotides. Specific uses are described for each of the 186 the new polypucleotides. Specific uses are described for each of the 186 the new polypucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW74848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 353-354; 721pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-506364/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bednarik DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1864 BP; 494 A; 403 C; 506 G; 455 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (see AAV59511 for described uses).
                                                                                                                                               11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 60
                                 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                           17
                                                                        61
                                                                                                                                                                  1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents a nucleic acid molecule designated Gene 120 the human cDNA clone HGBGZ64 (deposited as clone ATCC 97902 and 209048) which encodes a secreted human protein. The gene can be
                                                                                          eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1997;
                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DP, Brewer LA, Carter KC, Duan R, Ebner K, Ferrie AM, Fischer CL, Florence KA, Greene J Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, S, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z
                                                                                                                                                                                                                                                                                                                                   Ratio:
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97US-0056894.
97US-0056903.
97US-0056908.
97US-0056910.
97US-0056911.
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97US-0057761.
97US-0058785.
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                                                                                                                                                                                                                                                                                                                     Percent Identity:
                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                         97.917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endress GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA;
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:ABL32228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL32228 standard; DNA; 6049 BP
                                                                                                                                                                                                                                                                                                                                                                                                           WO200200928-A2
                                                                                             Claim 1; SEQ ID NO 201; 32pp + Sequence Listing; German
                                                                                                                                          Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                              Olek A,
                                                                                                                                                                                                                                                                                             01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                              30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                          02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                              cytosine methylation
                                                                                                                                                                                              WPI; 2002-130909/17.
                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCTGACTGGATCCACAGCAGTGGGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                                                            2000DE-1032529
                                                                                                                                                                                                                                    Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

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seq_documentation_block:
ID AAS00247 standard; DN
XX
AC AAS00247;
XX
DT 31-MAY-2001 (first &
XX
DT 31-MAY-2001 (first &
XX
DE Bcl-X1-DTR apoptosis-
XX
KW Human; Bcl-X1-DTR; ap
diphtheria toxin reck
KW hyper-proliferation;
KW transient ischaemic;
KW transient ischaemic;
KW Huntington's disease
XX
OS Chimeric - Corynebac;
OS Chimeric - Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAS00247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: ABL32228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-155-327E-9 x ABL32228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5401 TGGTTGATTGGATTTATAGTAGTGGGGGTTGG 5432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5351 ATTGGTGGGATAAGTGTAGGAGTGGATGGTGGTTTATTTGGAGACGTAGT 5400
                                                                                                        diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5151 GATGAGTTCGAGATTCGTTTTCGGCGTATTTTTTTTTGATTTGGCGGTTTA 5200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5101 GGGAGGGTTTAGTAGTTGATTCGTTGTATTAAGTTATGCGGGTAGTTGGA 5150
                                                 Chimeric - Homo sapiens
                                                                                              Huntington's disease.
                                                                                                                                                                              Human; Bcl-Xl-DTR; apoptosis; cancer; spinal muscular atrophy; ds;
                                                                                                                                                                                                                              Bcl-xl-DTR apoptosis-modifying fusion protein, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5051 TGTAGGTTATAAGTTGAGGTAGAAGGGTTATGTTTGTGGAGTTGGTTTCG 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5001 ATGGCGATTTTAGTTTCGGTTTTAGATATACGGGTTTTGGTGGTAGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                    AASO0247 standard; DNA; 1236 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6049 BP; 1480 A; 109 C; 1549 G; 2911 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTTTTGGGGTTGTATTGTGTGTTGAGAGTGTTAATAAGGAGATGGAATT 5350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
  Corynebacterium diptheriae Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438.00
3.744
81.250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 6049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 63.889
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alignment_block:

Percent Similarity:

63.090 429.50

Percent Identity: 39.485

Quality: Ratio:

Sequence 1236 BP; 317 A;

291 C; 343 G; 285 T; 0 other;

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CC The sequence represents the coding sequence of Bcl-Xl-DTR apoptosis-CC modifying fusion protein comprising human Bcl-Xl sequence fused via a CC short linker to diphtheria toxin receptor binding domain (DTR). The CC functional apoptosis-modifying fusion protein is capable of binding a CC target cell and integrating into or crossing a cellular membrane of the CC target cell and the Bcl-XL domain, which targets the fusion protein to the CC of the target cell. The fusion protein is useful for modifying confit or exponse CC (inhibiting or enhancing) apoptosis in a target cell, stem, tumour or CC lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or CC myper proliferative cell or an adipocyte. It is also useful for reducing capoptosis in a subject after transient ischaemic neuronal injury. CC especially spinal cord injury. The fusion protein may be used to treat cof apoptotic cellular response, including neurodegenerative disorders such as Alzheimer's disease, functing neurodegenerative disorders catrophy, stroke episodes and unregulated cell growth as in tumours and cord catively throughout the body and targeted to selective tissue and cc cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 54-56; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-218343/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU00219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Youle RJ, Liu X, Collier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HARD ) HARVARD COLLEGE.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-2000; 2000WO-US22293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200112661-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0149220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= d
/note= "Linker DNA, linking Bcl-x1 to DTR'
778..1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Bcl-Xl gene from codon 1-233"
760...777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "DTR, diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Bc1-x1-DTR fusion protein"
/note= "DTR is diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "10x Histidine tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
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US-09-155-327E-9 x AAS00247

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF75960
     E E X E X E X E X E X
                                                                                                                                                                                                                                                       seq_documentation_block:
ID AAF75960 standard; cDNA; 1742 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526 GACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 AGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 CGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGCAAAGCAAG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 AsnLysGluMetGluProLeuValGlyGlnValGlnAspTrpMetValAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476 GCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGGTAAACTGGGGTC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLysGlyTy 27
Rat Bcl-xL; apoptosis inhibitor; programmed cell death inhibitor;
wild-type; antiapoptotic; cell death-associated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 r..... 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 CGGGAGCTGGTTGACTTTCTCTCTACAAGCTTTCCCAGAAAGGATA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                   Rat wild-type Bcl-xL cDNA.
                                                                                                                                            22-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....ProLeuHisGlnA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 625
                                                                                                                                                                                                                                                                                                                                                                                                   CGTGGTTCTGCTGGGCTCACTCTTCAGTCGGAAAGCGTATTCTGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         yAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaSer 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: AAS00247 from: 1 to: 1236
                                                                                                                                                                                                                                                                                                                                                                                                            774
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alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-155-327E-9 x AAF75960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAF75960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a mutant rat Bcl-x protein and the cDNA encoding it. The mutant rat Bcl-x protein (Bcl-xrMK) has the substitutions Y22F, Q26N, and R165K relative to the wild-type Bcl-xL protein. The invention also encompasses recombinant vectors and host cells comprising the modified nucleic acid sequence. The mutant Bcl-x protein is able to permeate the cell membrane, thus enhancing its ability to be taken up into a cell and to act as an inhibitor of apoptosis (programmed cell death). Bcl-xFNK and nucleic acids encoding apoptosis in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in the cell in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue transplant preservative; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in additives for maintaining the stability of transplanted cells and organs. The present sequence represents cDNA encoding wild-type rat Bc1-xL.
                                                                                                                                                                                                                                                                                                                                    187 AAGAAACTGAACCAGAAAGGGAGACCCCCAGTGCCATCAATGGCAACCCA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 CAGCTGGAGTCAGTTTAGCGATGTCGAAGAGAACAGGACTGAAGCCCCAG 186
                                                                                                                                                                                                 237 TCCTGGCACCTGGCGGATAGCCCCGCGGTGAATGGAGCC...ACTGGCCA
                                                                      284 CAGCAGCAGTTTGGATGCGCGGGAGGTAATCCCCATGGCAGCAGTGAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLysGlyTy 27
44 lnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThr 60
                                                                                                                              uGlyProAlaAlaAsp.....ProLeuHisG 44
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1 AX022529 Sequence 6 from Patent
1 AX030817 Sequence 6 from Patent
1 AX030813 Sequence 8 from Patent
1 AX032531 Sequence 8 from Patent
2 AX030819 Sequence 201 from Patent
2 AX084240 Rattus norvegicus
2 AX084240 Rattus norvegicus
2 AX0845130 Sequence 201 from Patent
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i AF096291 Rattus norvegicus Bcl-
i U59747 Human Bcl-w (bcl-w) mRNz
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i U72350 Rattus norvegicus Bcl-x
i M754021 Sequence 6 from patent
AR118504 Sequence 1 from patent
AR124952 Sequence 1 from patent
AR144311 Sequence 39 from patent
AR172594 Sequence 6 from patent
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AJ001203 Sus scrofa mRNA for an
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1 U51278 Mus musculus thrus Bol
1 U25645 Gallus gallus bol-x (bo
1 AX085490 Sequence 1 from Pater
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                                AB073983 Canis familiaris mRN7
       BC019307 Homo sapiens, clone
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS MMU59746
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                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                            Quality: 1006.00
Ratio: 5.212
Percent Similarity: 100.000
                                                                                                                                                                                           Align seg 1/1 to: MMU59746
                                                                                                                                                                                                                                       US-09-155-327E-9 \times MMU59746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                             17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                        51 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                 Glbson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
bcl-w, a novel member of the bcl-2 family, promotes cell survival
Oncogene 13 (4), 665-675 (1996)
96358615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus Bcl-w (bcl-w) mRNA, complete cds. U59746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, po Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                         107
                                                                                                                                                                                                                                                                                                                                                                                                                          Product="B61-W"

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RLREGNWASVRTYLTGAVALGALVTVCAFFASK"

200 q 117 t
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/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="promotes cell survival; Bc1-2 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="bcl-w"
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421.50
417.50
412.50
411.00
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631.76
634.41
627.67
615.78
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Percent Identity: 99.482
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7.9e-27
5.7e-27
1.3e-26
6.2e-26
                                                                                                                                                                                                     to: 582
                                                                                                                                                                                                                                                                                                                           Length:
Gaps:
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U92434 Bos taurus bcl-2 mRNA
E I Z11961 G.domesticus mRNA fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E23357 Virus vector system x82537 R.norvegicus bcl-x
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seq_documentation_block:
LOCUS AF030769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 ACGAACTTTTCCAAGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 GCTACACGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACCCAGGTTTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GGGAAGGCCCAGCCGACCCGCTGCACCAACCCATGCGGGCTGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGCTGACTGGATCCACAGCAGTGGGGGGGTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                 Submitted (21-OCT-1997) Center for Molecular Medicine,
                                                                                                                                                                                                                                                                                                                       University,
                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                       Ross, A.J. and MacGregor, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MacGregor, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ross, A.J., Waymire, K.G., Moss, J.E., Parlow, A.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus BCL-W (Bcl-w) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-w is required for testis homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF030769.1 GI:2623249
                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 3476)
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                                                                                               /gene="Bcl-w"
                                                                                                                                          /map="
                                                                                                                                                                    /chromosome="14"
                                                                                                                                                                                                                /strain="C57BL/10J"
                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                               1462 Clifton Road, Atlanta, GA 30322, USA
                                                                                                                                             19.5 cm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3476 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Russell, L.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROD 16-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity: 100.000
               579
                         134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                         529
                                                                                                                                          117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                           479 GICTITGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                         101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                          429 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                                                                         379 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 GGGAAGGCCCAGCCGCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 328
                                                                                                                                                                                                                                                                                                                    84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                        67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG1 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 628
                                                                                               TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 1006.00
Ratio: 5.212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="mRNA destabilization element" 3428. 3441 /gene="BCl-w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number=3
179. .760
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171. .610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           991 g
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REFERENCE AUTHORS

TITLE AUTHORS

JOURNAL

REFERENCE

DEFINITION ACCESSION

451

401

351

301

SOURCE KEYWORDS VERSION

ORGANISM

FEATURES

exon gene

578

528

478

378

278

JOURNAL TITLE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-155-327E-9 x AR020779
                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
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JOURNAL
                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AR020779 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
201 GCTACACGTGACCCCAGGCTCAGCCAGCACGCTTCACCCAGGTTTCCG 250
                                                                                                                                             101 GGGAAGGCCCAGCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
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                                                                                                                                                                                                                                                        17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                   34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                          67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5/9 pp
Sequence 1 from patent US 5789201.
AR020779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes coding for bcl-y a bcl-2 homologue Patent: US 5789201-A 1 04-AUG-1998; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 579)
Guastella,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unknown"
157 c 198 g
                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity:
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                                                        alignment_scores:
                                                                                                               ORIGIN
                                                                                                                                    BASE COUNT
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF096291.1 GI:3747129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamner,S., Skoglosa,Y. and Lindholm,D.
Differential expression of bcl-w and bcl-x messenger RNA in the
developing and adult rat nervous system
Neuroscience 91 (2), 673-684 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-OCT-1998) Developmental New
University, Box 587, BMC, Uppsala 751 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hamner,S., Skoglosa,Y. and Lindholm,D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10366024
                       Quality: 1002.00
Ratio: 5.192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 582)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                                                                                                                              /note="Bcl-2 family member"
                                                                                                                                                                                                                                                                                                                                   /gene="bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 582
      Percent Identity: 98.964
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                                              Length:
                               Gaps:
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alignment_block:

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SOURCE
ORGANISM
        REFERENCE
                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
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                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                DEFINITION
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                                                                    TITLE
                          MEDLINE
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                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                            551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                  184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 GACGAGTTTGAGACCCGCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 GGGAAGGCCCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 nLeuHiSValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGCGACCCCAGCCTCAACCCCCAGACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProg 34
                   Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)
Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival 96358615
                                                                                                                                                                                                                                                                          Human Bcl-w (bcl-w) mRNA, complete cds. U59747
                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                               U59747.1 GI:1572492
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(bases 1 to 582)
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Percent Similarity: 100,000
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134 eualaaspTrpILeHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
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                                                                                                                                    351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                                                                                                                                117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                          301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                          101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 ACGAACTTTTTCAAGGGGGCCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 ASPGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGCATGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cory, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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/ DDOTEIN_1 d="AAB09055.1"

/ ABL_XTef="GI:1572493"

/ TITAL TITAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="promotes cell survival"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene-"bcl-w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 150
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167

GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGGCCCCTGG

151

seq_documentation_block:
LOCUS BC021198 seq_name: gb_pr:BC021198

SOURCE

ORGANISM

Homo sapiens

KEYWORDS VERSION

REFERENCE

TITLE

Direct Submission

(bases 1 to 1437)

JOURNAL AUTHORS

COMMENT

Web site:

nisc_mgc@nhgri.nih.gov http://www.nisc.nih.gov/

Zhang, L.-H. and Green, E.D.

NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP

ACCESSION DEFINITION

BC021198.1 GI:18203706

complete cds

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/organism="Homo sapiens"
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                                                                                                                       /tissue_type="Lung, small cell carcinoma"
/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
                                                                                                 /note="Vector: pOTB7"
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                                                                                                                                                                                                      /db_xref="taxon:9606"
                                                           /codon_start=1
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seq_documentation_block:

Human mRNA for KIAA0271 gene, complete cds.

3542 bp

mRNA

linear

PRI 06-OCT-2001

ACCESSION DEFINITION

D87461 D87461

D87461.1 GI:1944417

FEATURES

Location/Qualifiers

source

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pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCO21198 1437 bp mRNA linear PRI 22-JAN
Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Uch Stro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genemics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                          Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Shevchenko, Y., Wetherby, R.D., Beckstrom-Sternberg, S.M., Brooks, S., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Beossell, R., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Waduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 15 Row: k Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14574571
                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI 22-JAN-2002
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seq_name: gb_pr:D87461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 GGGAGGGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 ATGAACTITTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 475
                                                                                                                                                                                                                                                                                                                                                                                                  134 eualaaspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                     626
                                                                                                                                                                                                                                                                                              151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                            576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 evalGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                              84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                          726 TAACTGTAGGGGCCTTTTTGCTAGCAAG 754
                                                                                                         184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                   167
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                                                                                                                                                                                                             pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                         TGGCTGACTGGATCCACAGCAGTGGGGGGGGTTGGGGGGGAGTTCACAGCTCTA 625
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a 343 c 509 g 282 t
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Percent Identity: 98.446
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alignment_block:
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Percent Similarity: 100.000
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MEDLINE
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277
                                                                                                                                                                                    227 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                          177 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 226
                                                                                                                        34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                         17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                      1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
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                                                                                           GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohara, O., Nagase, T., Kikuno, R. and Nomura, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 3542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib:pSPORT 1 clone:HA6752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens male brain myloblast cell_line:KG-1 cDNA to mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     804
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RLREGGWASVRTYLTGAVALGALVTVGAFFASK"
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177. .7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="KIAA0271"
177. .758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to human transforming protein bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  997.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="KIAA0271"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_line="KG-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="HA6752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
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alignment_block:
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                                                                                                                                                                                        US-09-155-327E-9 x AR020780
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51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                   17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                                            1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     727 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       527 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427
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                                                                       ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACGGGGACGGGCCCTGGAGGAGGCCCCGGCGTCTGCGGGAGGGGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_pat:AR020780
                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes coding for bcl-y a bcl-2 homologue Patent: US 5789201-A 2 04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        579 bp
Sequence 2 from patent US 5789201.
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5.167
99.482
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154 c 208 g
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34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50

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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 6 from Patent EP0932674.
                                                                                                                                                                                                                                                                      Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. A novel mammalian gene, bol-w, belongs to the bcl-2 family of apoptosis-controlling genes patent: EP 0932674-A 6 04-AUG-1999; AMRAD OPERATIONS PTY LTD (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX022529.1 GI:10046125
                                                                                                                                                                                                                                                                                                                                                                                               unidentified
                                                                                                                                                                                                                                                                                                                                                                               unclassified
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Percent Similarity: 100.000
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                                                                                                                                                                                        seq_documentation_block:
LOCUS AX030817
                                                                                                                                                                                                                                    seq_name: gb_pat:AX030817
                                                   REFERENCE
                                                                                                     SOURCE
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                    TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                                                                                                                                                                                                                           551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                               184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGTCGACTGGATCCACAGCAGTGGGGGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                               GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                     583 bp
Sequence 6 from Patent W09735971.
AX030817
1 (bases 1 to 583)
Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
                                                                                                                                          AX030817.1 GI:10278311
                                                                      unclassified
                                                                                      unidentified
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400

linear

PAT 20-SEP-2000

JOURNAL

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AX030817 from: 1 to: 583
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501 GCCATCAGTGAGGACAGTGCTGACGGGGCCCGTGGCACTGGGGGCCCCTGG 550
                         167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                               451 TACGGGGACGGGCCCTGGAGGAGGCGCGCGCCTCTGCGGGAGGGGAACTG
                                                                                                                         151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                            401 TGGTCGACTGGATCCACAGCAGTGGGGGGTGGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                    134 eualaaspTrpIleHisSerSerGlyGlyTrpAlaGluPheThralaLeu 150
                                                                                                                                                                                                                                                                                          351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                                                                                                                                                                                                                                                                                                         301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                                                                                   101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 ACGAACTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 GCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTCTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGCCTCTGGTGGCAGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                      oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nLeuH1sValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAGGGCCAGCAGCTGACCGGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU); CORY SUZANNE (AU); GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)
LOCation/Qualifiers
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RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
a 157 c 210 g 111 t
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SOURCE
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ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_pat:Ax022531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                          151 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                          101 GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                   84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                              51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                             34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                       51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTG 100
                                                                                                                                                                                                                                                                                                                                              17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGCCGACCCCAGCCTCAACCCCCAGACACGCGCCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 581)
Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl.w, belongs to the bcl-2 family of apoptosis-controlling genes
Patent: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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5.142
98.446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 96.373
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seq_documentation_block: LOCUS AX030819
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                                                                                                                                      alignment_block:
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                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
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                                                                          Align seg 1/1 to: AX030819
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TACGGGGACGGGCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCATGAGTGAGCACAGTGGTGACGGGGGCCCGTGGCACTGGGGGGCCCCTGG 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8 from Patent W09735971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes patent: WO 9735971-A 8 02-OCT-1997;
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                                                                                                                                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unclassified.
                                                                                                                                                                                                Ratio:
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                                                                                                                                                                                                                                                                                                                 105 a
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5.142
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6
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                                                                                                                                                                                   96.373
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seq_documentation_block:
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                                                                                          COMMENT
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 eualaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 ValpheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 GGCATGAGTGAGCACAGTGGTGACGGGGGCCCTTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACGGGGACGGGCCCTGGAGGACGCACGGCGTCTGCGGGAGGGCCAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCTGACTGGATCCACAGCAGTGGCGGCTGGGCGGACTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 196292)

1 (bases 2 to 196292)

1 (bases 3 to 196292)

1 (bases 3 to 196292)

1 (bases 4 to 196292)

1 (bases 6 to 196292)

1 (bases 1 to 196292)

2 (Bases 1 to 196292)

2 (Bases 1 to 196292)

2 (Bases 1 to 196292)

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9 (Bases
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Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11
                                                                            - Web : www.genoscope.cns.fr)
on Jun 3, 2000 this sequence version replaced gi:6138746
                                                                                                                                                                  Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL049829.4 GI:8217859
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from chromosome 14 of Homo sapiens (Human), complete sequence
                                                                                                                                                                                                                                                                                                              Genoscope
Center: Genoscope / Centre National de Sequencage
                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                              (bases 1 to 196292)
                                                          -- Genome Center
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Overall quality chart :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: Phrap; version 2.0 Quality coverage: 7.94x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.genoscope.cns.fr/
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- 29
- 39
- 59
- 79
                                   128419. .128543
/note="matching EMBL:R87257
RHdb:RH53698
                   dbsts:sts18321
                                                                        Identified using the e-PCR software (G. Schuler)"
                                                                                                   dbSTS:STS25817
                                                                                                                     RHdb: RH53520
                                                                                                                                                     Identified using the e-PCR software (G. 128387. .128525
                                                                                                                                                                                     dbSTS:STS40201
                                                                                                                                                                                                        RHdb:RH47139
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                                                                                                                                                                                                                                                                          dbsts:sts45044
                                                                                                                                                                                                                                                                                                                                                           dbSTS:STS52191
                                                                                                                                                                                                                                                                                                                                                                           /note="matching EMBL:AA007328 RHdb:RH75103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identified using the e-PCR software (G. Schuler)"
82164. . 82299
/note="matching EMBL:H79035
                                                                                                                                 note="matching EMBL: H22648
                                                                                                                                                                                                                   /note="matching EMBL:D11677
                                                                                                                                                                                                                                                                                                                                                                                                                                             dbSTS:STS55514
                                                                                                                                                                                                                                                      Identified using the e-PCR software
                                                                                                                                                                                                                                                                                                    /note="matching EMBL:R94929
                                                                                                                                                                                                                                                                                                                             107758.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dbSTS:STS68485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="matching EMBL:AA908790 RHdb:RH102162
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [dentified using the e-PCR software (G. Schuler)"
30433. .80566
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                                                                                                                                                                   Schuler) "
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US-09-155-327E-9 x CNS0000B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: CNS0000B from: 1 to: 196292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                 90026 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 90075
                                                                                                                   89976 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 90025
                                                                                                                                                                                   89876 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 89925
                                                                                                                                                                                                                                                                                                                        89826 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 89875
84 spGluLeuPhcGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhcPhe 100
                                                               67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                          17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dbSTS:STS48564
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RHdb:RH28671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identified using the e-PCR software 138568. .138647 the="matching EMBL:M78986"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schuler)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schuler)"
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90126 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGTGGAACC 90175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90176 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCAGC 90225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90226 TGGCTGACTGGATCCACAGCAGTGGGGGCTGGGTAAGAAGCTTCTCAATT 90275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90426 TCCAGGGCTGCCATGCAGTCAACACTGGATGGGCTCATGGTCCCAAGCAG 90475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90376 AGTCTCCCCGTCTGGATGGAATTAGATTGAGAGATGCCTGGACTCTGCAC 90425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90326 GCTCTGATTGGAGGCTGAGGCAGCTATGTTGGGAATGAGGTACGGGGCTG 90375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90276 GCCGCTCTGCACATCCTTCTGCAAAGCTGGTCTCCAGGGGGAAGATGGGG 90325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90526 CTTTTTACATCTGAGTCATGGCGTGGGAGGTGGGGAGGACCAGGGATGGG 90575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90476 AGGACAGAATACACACCCAAGGAGTGCCTGCAGGGGAATGTTGTCAGGGA 90525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90576 TGGTGGTCAGGCAAGCCTTGGCAAAGGATGCTAGTTCTGAGCAGAATTTT 90625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90676 AGTCTCTCAGGGTGGGGGTGCACCTGGGGGGGATCAGAGGGGCCTTGCAGGG 90725
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                                                                                                                                                                                                                                                                                                                                                                                                                              90726 AGAAGAGCTTTGGCCAGAGAGGAGCTGGGTATGGGGTAGTGCTCGCAGTG 90775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                  90926 TGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTG
                                                                                                                                                                       90826 GATATCCCTTTCTCCTTCTTTCTCTCCTGCTTCCCTTCTCTCCCACAGGC 90875
                                                                                                                                                                                                                                                                                                                                           90776 GATGGAACTGGAACTCTTCCTCTCTCTCTCTCCACTCTTTCCTCTCT 90825
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                                                                                                                                                                                                                                                                                                145 ......Ala 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 ...... 144
                                      179 AlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaSerLys 193
                                                                                                         162 euArgGluGlyAsnTrpAlaSerValArgThrValLeuThrGlyAlaVal 178
.GluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArgL 162
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                     FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Ho,S.-L., Idol,J., Karlins,E., Lee-Lin,S.-Q., Legaspi,R., Lim,M.,
Maduro,Q.L., Maduro,V.B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Prasad,A., Snyder,B., Stantripop,S.,
Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D. and Green,E.D.
NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Norway, WORKING DRAFT SEQUENCE, 5 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On NOV 8, 2000 this sequence version replaced gi:10179358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 151212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 151212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing vector: plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 147800 bases at least 040 consensus quality: 148726 bases at least 030 consensus quality: 148733 bases at least 020 consensus quality: 149333 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 145000; agarose-fp
Insert size: 150812; sum-of-contigs
Quality coverage: 11.76x in Q20 bases; agarose-fp
Quality coverage: 11.30x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: 2468
Center clone name: 2468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                20441
20541
41010
41110
65553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.nisc.nih.gov
                                                                                                                                                                                       65653
/strain="Brown Norway"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---- Genome Center
                                                  /organism="Rattus norvegicus"
                                                                                                        Location/Qualifiers
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    Summary Statistics

                                                                                                                                 65652: gap of unknown length
110365: contig of 44713 bp in length
110465: gap of unknown length
151212: contig of 40747 bp in length
                                                                                                                                                                                                                                      41109: gap of unknown length 65552: contig of 24443 bp in
                                                                                                                                                                                                                                                                                         20440: contig of 20440 bp in length 20540: gap of unknown length 41009: contig of 20469 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151212 bp
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4 clone RP31-246H18 strain Brown
                                                                                                                                                                                                                                                  length
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alignment_block:
US-09-155-327E-9 x AC079885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AC079885 from: 1 to: 151212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 86.528
                                                                74915 TGGCTGACTGGATCCACAACAATGGGGGCTGGGTGGAGTTCACAGCTCTA 74964
                                                                                                                                                                                                                                                                                                                                                                                                      74865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74715 GCTACATGTGATGCCAGGCTCAGCCCAACAATGCTTCACCCAGGTTTCCA 74764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74665 GACAAGTTAGAGACCCACTTCCAGCACACCTTCTCTGGACCTGGCCACTCA 74714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74615 GGGAAGGCCCAACAGCCAACCTGATACACCAAGCCATGTGGGCTGCTGGA 74664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74605 .....GCTGGCCCCG 74614
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                                                                                                                                                                                                                                                                                           117
                      167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                       134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                      151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                            101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                            OLeuValGlyGlnValGlnAspTrpMctValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                     ATTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCCAGAGACACGCC 74914
                                                                                                                                                                                                                                                                                                                        GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAGAAAAATAGAGCC 74864
/note="assembly_fragment"
43370 a 30838 c 31177 g 45417 t
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4.036
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65653. .110365
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clone_end:SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib-"RP31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP31-246H18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="4"
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_htg:AC084240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75065 TAACTGTAAGGGCCTTTTTTACTAACAAG 75093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75015 GGCATCAGTGAGGACAATACTGACTGGGGCTGTGACACTGGGGACCCTGA 75064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
Bouffard,G.G., Brinkley,C., Dietrich,N.L., Gupta,J., Ho,S.-L.,
Idol,J., Lee-Lin,S.-Q., Legaspi,R., Lim,M., Maduro,O.L.,
Maduro,V.B., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
Pearson,R., Prasad,A., Snyder,B., Stantripop,S., Thomas,J.W.,
Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tran,J.T., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D. and Green,E.D.
NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 179798 bases at least 040
Consensus quality: 180132 bases at least 030
Consensus quality: 180274 bases at least 030
Consensus quality: 180274 bases at least 020
Insert size: 138000; agarose-fp
Insert size: 160000; pulse-field-gel
Insert size: 160982; sum-of-contigs
Quality coverage: 15.02x in 020 bases; agarose-fp
Quality coverage: 11.45x in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT.
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Norway, WORKING DRAFT SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                                     be preserved.
                                                                                                                                                                                                                                                as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 181282)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 181282)
                                                              5431
5531
39504
39604
85793
                             85893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- Summary Statistics
Location/Qualifiers
           5430: contig of 5430 bp in length
5530: gap of unknown length
39503: contig of 33973 bp in length
39603: gap of unknown length
85792: contig of 46189 bp in length
85892: gap of unknown length
181282: contig of 95390 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Center
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BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-155-327E-9 x AC084240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 4.036
Percent Similarity: 86.528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AC084240 from: 1 to: 181282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49782 ATGGCAACCCCAACCTCAATCCCAGACACATGGGCTCTAATGGTTGA... 49828
                                                                                                                                                                                                                                                                                                                                                                                                                                                49989 ACGAACTTTTCCAAGGGGGCCCCAACTAGGGCCATCTTGTGACATTCTTT 50038
                                                                                                                                                                                                                                                                           49939 GCTACATGTGATGCCAGGCTCAGCCCAACAATGCTTCACCCAGGTTTCCA 49988
                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                       151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                         67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100 ::|||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
||||||||||||::::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50811 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .181282
/organisme"Rattus norvegicus"
/strain="Brown Norway"
/db_xref="taxon:10116"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
85893. 181282
/note="assembly_fragment"
1 36290 c 37296 g 56560 t
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39604. .85792
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4.036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP31-103L21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RP31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .5430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .39503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 69.948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 others
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Sequence Strd Orig Zescore Escore Lend | Document at D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 About: Results were produced by the GenCore software, version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MODEL-frame-p2n.model -DEV=xlh
-Q-cgn2_1/USPTO_spool/US09155327/runat_06062002_084852_18504/app_query.fasta_1.508
-Q-cgn2_1/USPTO_spool/US09155327/runat_06062002_084852_18504/app_query.fasta_1.508
-DB-Issued_Patents_NA -QPMT-fastap -SUFFIX-P0n.rni
-DB-Issued_Patents_NA -QPMT-fastap -1.00 -LOOPCL-0.000
-CAPDP=12.000 -GAPEXT-4.000 -MANATCH=0.100 -LOOPCL-0.000
-LOOPEXT=0.000 -GAPEXT-4.000 -YGAPEXT-7.000 -YGAPEXT-10.000
-YGAPEXT-0.500 -FGAPOP-4.500 -PGAPEXT-7.000 -YGAPEXT-10.000
-YGAPEXT-0.500 -DELOP=6.000 -DELEXT-7.000 -START-1
-YGAPEXT-0.500 -DELOP=6.000 -THR_MIN-0 -ALIGN=200
-MANTRIX-DIOSUM62 -TRANS-human40.cdi -LIST-45 -DOCALIGN=200
-MANTRIX-DIOSUM62 -THR_MAX-100 -THR_MIN-0 -ALIGN=15 -MODE-LOCAL
-PHR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -MAXIEN-200000000
-USTENT-DFS -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXIEN-200000000
-USTENT-DFS -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXIEN-2000000000
-USTENT-DFS -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXIEN-2000000000
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Database length: 122816752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search time (sec): 65.480000
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length: 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_NA:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US94-07089-8 + 183
/cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-471-058-6 + 176.00
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-944-530-1 + 176.00
/cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-471-057-6 + 176.00
/cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-471-058-8 + 173.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-798-897-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08798897 Patent No. 5789201
                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-798-897-2
                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-798-897-2 from: 1 to: 579
                                                                                                                                                                                                                                                                                          US-09-155-327E-7 \times US-08-798-897-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Genes Cod
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTIN KEL
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                   ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Esmond, Robert W. REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: Februa
                                                                                   34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                      51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                        17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-3/1-2540
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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99.482
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                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 99.482
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340.26 2.9e-11 20

340.26 2.9e-11 20

340.26 2.9e-11 20

340.26 2.9e-11 20

339.41 3.2e-11 12
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5883229
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08978523 Patent No. 5883229
                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Codi
TITLE OF INVENTION: Homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: herew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            20005
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IBM PC compatible
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N: 424
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                                                                                                                    32,893
                                                                                               1483.0140002
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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-798-897-1
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                            551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                     184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                          501 GGCATCAGTGACGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCCTGG
                                                                                        167 pAlaServalArgThrvalLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                         151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                            451 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                              351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                           117 oLeuvalGlyGlnvalGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                               67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
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TYPE: nucleic
STRANDEDNESS:
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DEDNESS: both
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seq_documentation_block:

Sequence 1, Application US/08798897 Patent No. 5789201 GENERAL INFORMATION:

APPLICANT:

Guastella, John

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; MOLECULE TYPE: cDNA US-08-798-897-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                      151 GACGAGTTTGAGACCCGCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                           101 GGGAAGGCCCAGCCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
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CITY: Washington
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                             101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                251 ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300
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                                                                                                                                   34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: bot
                                                                                                                                                                                                                                     51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                   84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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20005
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Esmond, Robert W.
Esmond, Robert W.
32,893
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/08978523 ; Patent No. 5883229
                                                                                                ; MOLECULE TYPE: US-08-978-523-1
                                              alignment_scores:
percent Similarity: 100.000
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                                                                                                                                                                                                                  TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 1:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/978,523
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                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                    LENGTH:
                 Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                            US 08/798,897
                                                                                                                                                                                                                                                                                                   32,893
     percent Identity: 98.446
                                                                                                                                                                                                                                                                                            1483.0140002
                                          Length:
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alignment_block: US-09-155-327E-7 x US-08-978-523-1

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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-081-448-5
                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08081448 Patent No. 5646008
                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Thompson, Craig B.

APPLICANT: Boise, Lawrence H.

TITLE OF INVENTION: Compositions and Methods

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-978-523-1 from: 1 to: 579
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 GCCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 TGGCTGACTGGATCCACAGCAGTGGGGGGGGGGGGGGGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 eualaaspTrpIleHisSerSerGlyGlyTrpAlaGluPheThralaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                                                                 STREET: 321 No
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCCAGGTTTCCG 250
                                                        ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 GACGAGTTTGAGACCCGCTTCCGGCGCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                         COUNTRY:
                                                                                                   STATE:
                                                                                                                               ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5646008th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 GGGAAGGCCCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProg 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 428.50
Ratio: 3.018
Percent Similarity: 63.393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-155-327E-7 x US-08-081-448-5
550 GCATTGTGGCCTTTTTCTCCTTCGGCGGGCACTGTGCGTGGAAAGCGTA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312-755-4489
INFORMATION FOR SEQ ID NO:
                                                                     500 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTC
                                                                                                                                                                                                                     350 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGCAAG
                               95 rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
                                                                                                                                                                                                                                                                                                                                                                        300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                               250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
                                                                                                    78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                                                                  62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 CGGGAGCTGGTTGACTTTCTCTCCTACAAGCTTTCCCAGAAAGGATA 199
                                                                                                                                                                                                                                                                                                                                  41 .....ProLeuHisGlnA 45
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 .....ValCysGlyAlaGlyPro 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 312-744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646008thrup, Thor
REGISTRATION NUMBER: 33 268
REFERENCE/DOCKET NUMBER: ARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448
FILLING DATE: 19390622
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-470-670A-6
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alignment_scores:
Quality:
Ratio:
                                                                                                          US-08-470-670A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08470670A Patent No. 5834309 Patent No. 5834309 5710045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600 GACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCAC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AsnLysGluMetGluProLeuValGlyGlnValGlnGluTrpMetValAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       700 ATACTITTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: VERFEBBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       800 CGTGGTTCTGCTGGGCTCACTC 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: AR
TELECOMMUNICATION INFORMATION:
TELECHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/081,448
APPLICATION NUMBER: US 08/081,448
                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/470,670A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                          LENGTH: 926 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                             Highlander, Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
                                                                                                                                  CDS
135..836
                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                       single
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428.50 3.018

Length:

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-155-327E-7 \times US-08-470-670A-6
     Sequence 1, Application US/08481739
; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
APPLICANT: June, Carl H. and Thompson, Craig B.
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-481-739-1
                                                                                                                                                                                   seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 CGCTGAGGGAGGCGACGAGTTTGAACTGCGGTACCGGCGGCATTC 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600 GACAAGGAGGTAGTTGGTGAGTCGGATCGCAGCTTGGATGGCCAC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 AsnLysGluMetGluProLeuValGlyGlnValGlnGluTrpMetValAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
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                                                                                                                                                                                                                                                                                     800 CGTGGTTCTGCTGGGCTCACTC 821
                                                                                                                                                                                                                                                                                                                                       176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                                                         750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
                                                                                                                                                                                                                                                                                                                                                                                                                                         162 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
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NUMBER OF SEQUENCES:
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CORRESPONDENCE ADDRESS:

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alignment_block:
US-09-155-327E-7 x US-08-481-739-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 3.105
Percent Similarity: 61.333
                                      397 AAGCGCTGAGGGAGGCGACGACTTTGAACTGCGGTACCGGCGGGCA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                 347 CAGCAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGC 396
                                                                                                                                                                                            300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCC...ACTGGCCA 346
                                                                                                                                                                                                                                                                       250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                                                                                                                                                  200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
                                                                                                                                                                                                                                                                                                                                                                                                                             150 CGGGAGCTGGTTGACTTTCTCTCCTACAAGCTTTCCCCAGAAAGGATA 199
61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
                                                            44 lnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThr 60
                                                                                                                                                     35 uGlyProAlaAlaAsp.....ProLeuHisG 44
                                                                                                                                                                                                                                                                                                           27 ...... 27
                                                                                                                                                                                                                                                                                                                                                                                      11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
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LENGTH: 926 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/481,739
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/435,518
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELECOMMUNICATION INFORMATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: DeConti, Giulio A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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135..836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : (617)227-7400
: (617)742-4214
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alignment_block:
US-09-155-327E-7 x US-09-167-921-1
                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (135)..(836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1
                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                           Align seg 1/1 to: US-09-167-921-1 from: 1 to: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
; Sequence 1, Application US/09167921A
; Patent No. 6172216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-167-921-1
                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nickoloff, Brian J.

APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0324
CURRENT FILLING DATE: 1998-10-07
CURRENT FILLING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SCOTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           797 CGGCGTGGTTCTGCTGGGCTCACTC 821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   747 AAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGC 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 ArgLeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuTh 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 rpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 ValAsnLysGluMetGluProLeuValGlyGlnValGlnGluTrpMetVa 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              547 GTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGCACTGTGCGTGGAAAGC 596
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                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                          428.50
3.018
63.393
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FILE REFERENCE: 159H-0339
CURRENT APPLICATION NUMBER: US/09/277,020
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-277-020-39
                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
TITLE OF INVENTION: Of mRNA Processing
                                                                                                                                                                                                                                                                                                         Sequence 39, Application US/09277020 Patent No. 6210892
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ENGTH: 926
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; ORGANISM: Homo sapiens US-09-277-020-39
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US-09-155-327E-7 x US-09-277-020-39
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seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-323-743-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                          145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
                                        800 CGTGGTTCTGCTGGGCTCACTC 821
                                                                            176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                  750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
                                                                                                                                                  162 LeuargGlu......GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
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3.018
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seq_documentation_block:

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alignment_block:
US-09-155-327E-7 x US-09-323-743-1
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; LOCARTON: (135)..(836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-323-743-1
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LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
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500 CTTTGAACAGGTAGTGAATGAACTCTTCCCGGATGGGGTAAACTGGGGTC 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILLING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILLING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILLING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Shang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0368
                                                                                       450 AGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAG 499
                                                                                                                                                                              400 CGCTGAGGGAGGCAGGCGAGTTTGAACTGCGGTACCGGCGGGCATTC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                        350 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGCAAG 399
                                                                                                                                                                                                                                                                                                                                                                  300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG 349
                                      78 gPheThrGinValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                   62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                          45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                                  41 .....ProLeuHisGlnA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 CGGGAGCTGGTTGACTTTCTCTCCTACAAGCTTTCCCCAGAAAGGATA 199
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                                                                                                                                                                                                                                                                                                                                                                                                            27 F....... 27
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3.018
63.393
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US-08-461-511A-6
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    Sequence 6, Application US/08461511A
    Patent No. 6303331
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-461-511A-6
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: ARCD:179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          800 CGTGGTTCTGCTGGGCTCACTC 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         750 GCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600 GACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCAC 649
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            SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thompson, Craig B.B.

Boise, Lawrence H.

TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                       LENGTH: 926 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                  NAME/KEY: CDS
LOCATION: 135..836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/461,511A
FILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN
                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Houston
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alignment_scores:

Quality: 428.50

Length:

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alignment_block:
US-09-155-327E-7 x US-08-461-511A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-461-511A-6 from: 1 to: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCCAG 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 .....valCysGlyAlaGlyPro 33
                                                                                  seq_name: /cgn2_6/ptodata/1/ina/pcTuS_COMB.seq:pcT-uS94-07089-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGCAAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 .....proLeuHisGinA 45
                                                                                                                                                                                                                                                                                                                                                                                                                           45 lametArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                                                   62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                                                                                                                                                                               500 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTC 549
                                                                                                                                                                                                                                                                                                                                                                                                   78 gpheThrGlnValSerAspGluLeupheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                                                                                                                                                                                             112 AsnLysGluMetGluProLeuvalGlyGlnValGlnGluTrpMetValAl 128
                                                                                                                                                                                                                                                                                        600 GACAAGGAGATGCAGGTATTGGTGAGTCGGAATCGCAGCTTGGATGGCCAC 649
                                          Sequence 6, Application:
                                                                                                                                                                                                                                                                 128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
                                                                                                                                                                                                                                              650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
                                                                                                                                                                                                  700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGAGCCGAAAG 749
                                                                                                                                                                                                                      145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                          162 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                       750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
                                                                                                                                 176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                           800 CGTGGTTCTGCTGGGCTCACTC 821
APPLICANT:
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 9
                                                         Application PC/TUS9407089
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alignment_scores:
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US-09-155-327E-7 x pcT-US94-07089-6
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OPERATING SYSTEM: PC-DA
OPERATING SYSTEM: PC-DA
CURRENT APPLICATION NUMBER: PC'
APPLICATION NUMBER: PC'
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: P.O. BOCITY: Houston STATE: TX
                                                                                                                                                                                                                                                                                                                                                          percent similarity:
                                                                                                                                                                                                                                                                                                Align seg 1/1 to: PCT-US94-07089-6 from: 1 to: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 713-789-26/9
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT DAVID L.
NAME: PARKER, DAVID L.
NAME: PARKER, 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: 512-320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: PAKAGEN, 32, REGISTRATION NUMBER: REFERENCE/DOCKET NUMBER: REFERENCE/TON INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 926 base pairs
TYPE: nucleic acid
TYPE: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                      11 ArgAlaLeuValAlaAspPheValGlyTyTLysLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                         200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
                                                                                                                                                              250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                               27 F...... 27
                                                                                                               300 TCCTGGCACCTGGCAGACAGCCCCGGGTGAATGGAGCC...ACTGGCCA 346
                                                                   347 CAGCAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGC 396
                                                                                                                                                                                   27 ...... 27
                                                                                                                           35 uGlyProAlaAlaAsp.....proLeuHisG 44
                                           44 inAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThr 60
61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
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Ratio:
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E: Floppy disk
E: Floppy disk
SYSTEM: PC-DOS/MS-DOS, ASCII
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135..836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 JUNE 1993
                                                                                                                                                                                                                                                                                                                                                                   428.50 Length: 2.4
3.105 Gaps:
61.333 Percent Identity: 41.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/081.448
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APPLICATION NUMBER: US 08/124,256
PRIOR APPLICATION DATA:
PILING DATE: 20-58P-1993
APPLICATION DATA:
PILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/840,716
PRIOR APPLICATION DATA:
PILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/288,692
APPLICATION NUMBER: US 07/288,692
APPLICATION NUMBER: US 07/288,692
APPLICATION NUMBER: 34.600
REFERENCE, DOCKET NUMBER: 34.600
TELECHONUMICATION THEORNATION:
PRICE PROMOMINICATION THEORNATION:
TELEPHONE: (408) 436-2070
TELEPHONE: (408) 436-2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: TYPE: FORM:

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,485A

CLASSIFICATION: 514

APDITATION: 514
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Sequence 20, Application US/08465485A
Patent No. 5831066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: 20
CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-465-485A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/124,256
TELEFAX: (408) 436-2075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 rGlyAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   747 AAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGC 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 ArgLeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuTh 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  697 GGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCAGCCGAGAGCCGA 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 rpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 valAsnLysGluMetGluProLeuvalGlyGlnValGlnGluTrpMetVa 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 lyArgLeuValAlaphePheValPheGlyAlaAlaLeuCysAlaGluSer 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 TTCAGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 nArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpG 94
                                                                                            3335-070-55 CONT
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seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-09-080-285-20
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; Sequence 20, Application US/09080285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6040181
GENERAL INFORMATION:
                                                alignment_scores:
                                                                                                     US-09-080-285-20
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           616 ATGCGGCCTCTGTTTGATTTCTCCTGGCTGTCTCTGAAGACTCTGCTCAG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666 TTTGGCCCTG...GTGGGAGCTTGCATCACCCTGGGTGCCTATCTGAGCC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 rGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   713 ACAAG 717
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                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, John TITLE OF INVENTION: Regulation of bcl-2 Gene Expression NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
EILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 22-DEC-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
                                                                                                                                                          FEATURE:
                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/840,716 FILING DATE: 21-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/124,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/080,285
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                 Quality:
                                                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                          Fortney, Andrew D
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1755 S. Jefferson Davis Hwy., Suite 400
                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                 : (408) 436-2070
(408) 436-2075
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                                                                                                                        1..717
                                                                                                                                         CDS
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22-DEC-1988
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   59.574
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                    2.932
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   Percent Identity: 37.021
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                                         Length:
                          Gaps:
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alignment_block:
US-09-155-327E-7 x US-09-080-285-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 CCCCGCACCGGGCATCTTCTCCTCCCAGCCCGGGCACACGCCCCATCCA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 TGCCCCGGCGCCGCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGG 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 .....proGlyGlu...... 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 GGGCTACGAGTGGGATGCGGGAGATGTGGGGCGCCGCGCGCCCCGGGGGCCG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 GAGAGCGTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTG 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 GluSerValAsnLysGluMetGluProLeuValGlyGlnValGlnGluTr 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 euHisGlnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArg 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 ...... GlyProAlaAlaAspPro...... 42
                                                                                                                                                                                              175 rGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaS 192
                                                                                                                                                                                                                                               616 ATGCGGCCTCTGTTTGATTTCTCCTGGCTGTCTCTGAAGACTCTGCTCAG 665
                                                                                                                                                                                                                                                                                          159 AlaArgArgLeuArgGluGlyAsnTrpAlaSerValArgThrValLeuTh 175
                                                                                                                                                                                                                                                                                                                                              578 GAGGCTGGGATGCCTTTGTGGAACTGTACGGC......CCCAGC 615
                                                                                                                                                                                                                                                                                                                                                                                          142 lyGlyTrpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGlu 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 pMetValAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 snTrpGlyArqLeuValAlaPhePheValPheGlyAlaAlaLeuCysAla 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 ArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAl 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 ASpThrArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLy 25
                                                                                                                                                666 TITGGCCCTG...GTGGGAGCTTGCATCACCCTGGGTGCCTATCTGAGCC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 aGlnGlnArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProA 92
                                                      713 ACAAG 717
                                                                                                      192 erLys 193
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seq_documentation_block:

SEQUENCES

NUMBER OF SEQUENCES: 4

;Patent No. 5459251
; APPLICANT: Tsujimoto, Yoshide;Croce, Carlo A.
; TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE

alignment_block: US-09-155-327E-7 x 5459251-1 alignment_scores: 5459251-1 Align seg 1/1 to: 5459251-1 from: 1 to: 4825 Percent Similarity: ;SEQ ID NO:1: 1986 GATGACTGAGTACCTGAACCGGCACCTGCACACCTGGATCCAGGATAACG 2035 59 ArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAl 75 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/228,704

FILING DATE: 18 APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 994,941

FILING DATE: 23-DEC-1992

APPLICATION NUMBER: 663,010

FILING DATE: 19-MAR-1991

APPLICATION NUMBER: 883,687

FILING DATE: 09-JUL-1986 142 lyGlyTrpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGlu 158 125 pMetValAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerG 142 1636 GCCGCATCCCGCGACCCGGTCGCCAGGACCTCGCCGCTGCAGACCCCGGC 1685 1586 CCCCCGCACCGGGCATCTTCTCCTCCCAGCCCGGGCACACGCCCCCATCCA 1635 92 snTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAla 108 36 GlyProAlaAlaAspPro..... 42 25 sGlyTyrValCysGlyAlaGly......32 9 AspThrArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLy 25 LENGTH: 4825 Quality: 410.50 Ratio: 2.932 milarity: 59.574 Gaps: 5
Percent Identity: 37.021 : Length:

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OM of: US-09-155-327E-7 to: EST:* out_format : pfs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: Jun 6, 2002
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gb_est2:BE508939
gb_est2:BG677345
gb_est1:AW326901
gb_est1:AW326901
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-DB-EST -QFMY=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -QGAPEXT=4.000
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-DELEXT=7.000 -TRANS-human40.cdi
-DELEXT=7.000 -TRANS-human40.cdi
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Database length: -1841457050
Search time (sec): 2329.970000
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gb_est1:AL632408
gb_est2:BM457276
gb_est2:BE293685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est2:B1764428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est2:BI910270
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955.00 1991.02
953.00 1991.48
890.00 1787.30
761.00 1523.93
758.50 1521.74
740.50 1482.88
731.00 1467.99
783.00 1164.56
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1999.72
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1145.71
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1026.93
987.92
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8.2e-102
2.0e-97
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1.6e-72
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1.9e-54
1.4e-54
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2.8e-34
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1.1e-32
8.8e-33
1.4e-32
2.6e-32
4.5e-32
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1.2e-33
2.4e-33
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5.9e-48
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AK015644 Mus musculus adult ma

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i BE793530 601590016F1 NIH_MGC_7

i AL157542 DKFEP761D0816_F1 761

i BI770566 603060362F1 NIH_MGC_13

i BI770564 Mus musculus 10, 11 da

i BI310270 603069493F1 NIH_MGC_11

i BF785386 602111728F1 NIH_MGC_14

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i BG288789 602396527F1 NIH_MGC_94
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BG831301 60276613221 NIH_MGC_12
BG824757 60272874521 NIH_MGC_15
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      BJ060637 BJ060637 NIBB MOCHET R
BG180671 602329448F1 NIH_MGC_91
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gb_est2:BF569393
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Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Koya,S.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Saito,H., Saito,R., Sakai,C., Sakai,R., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
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Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, Clone_lib:RIKEN full-length enriched mouse cDNA library
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The RIKEN Genome Exploration Research Group Phase II Team and the
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Submitted (10-JUL-2000) voshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoh
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                            Tsurumi-ku, Yokohama
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                                                   232 GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 281
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                                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG1 67
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Ratio: 5.181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="bab29912.1"
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132. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 GCCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGGCCCCTGG 681
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Shikawa, T., Okazaki, Y., Shikawa, T., Shikawa, Y., Shi
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High-efficiency full-length cDNA cloning
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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polyA_site
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5 (bases 1 to 3487)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="lung"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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/translation="ManPaSFPDTRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQ
/transl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409
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                                                                                                 human.
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COMMENT

TITLE

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Align seg 1/1 to: AK004680 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 100.000
                                                                                                      seq_name: gb_est2:BE793530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                      117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                        559 TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                            151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                         709 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                       167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG 458
                                                                                                                                                                                                                                                                          TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 1000.00
                                          BE793530 1030 bp mRNA linear EST 20-SEP-
601590016F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5',
                                 mRNA sequence
BE793530.1 GI:10214832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          777 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            834 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 98.964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 3487
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alignment_block;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: BE793530 from: 1 to: 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-155-327E-7 x BE793530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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394 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCCCCTTGTAGCCTTCTTT 443
                                                                                                       344 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 393
                                                                                                                                                                                                                                      294
                                                                                                                                                                                                                                                                                                                 244 GGGAGGGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA 293
                              84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                         194 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 193
                                                                                                                                   67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                        51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                               GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM800 row: p column: 04
High quality sequence start: 5
High quality sequence stop: 709.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1030)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DHIOB (phage-resistant)"
/note="Organ: lung: Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; cDNA made by oligo-dT prinning. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
chalaboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 284 c 386 g 170 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3944307"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 97.368
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alignment_scores:
                                                                                                                                                        BASE COUNT
                                                                                                                                        ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est1:AL157542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                644 GCCATCAGTGAGGACAGTGCTGACGGGGGGGGGGTGGCACTGGGGGGGCCTGG 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu. 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       694 GTAACTGTAGGGGCCTTT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 ValThrvalGlyAlaPhe 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    594 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGGAGGGGACTG 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                              Quality:
                                                                                                                                                                                                                                                                                                                                                           Berlin-Charlottenburg, GERMAN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (Buropean Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                       Please contact the RZPD: Ressourcenzentrum,
                                                                                                                                                                                                                                                                                                                                                                                                                   No s1 sequence available.
This clone (DKFZp761D0816) is available at the RZPD in Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 804)
Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Ansorge W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKF2p761D0816_r1 761 (synonym: h
DKF2p761D0816 5', mRNA sequence.
AL157542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                           Ratio:
                                                                                                                                                        150
4.964
99.482
                                                                                                                                        /lab_host="DH10B"
/note="Vector: pSportl; Site_1: NotI; Site_2: SalI"
/ 217 c 294 g 142 t 1 others
                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP761D0816"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
                                            953.00
                                                                                                                                                                                                                                                                                                                                                                                  GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       804 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hamy2) Homo sapiens cDNA clone
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Percent Similarity:

Percent Identity: 99.482

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alignment_block:
US-09-155-327E-7 x AL157542
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                                                                                                                                                                                                                                                                                                                            seq_name: gb_est2:BI770566
                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                         SOURCE
                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                           DEFINITION
                                 COMMENT
                                                                                                      REFERENCE
                                                                                                                                                        ORGANISM
                                                                    TITLE
                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGCAGCTGGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ValpheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 1yGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 TACGGGGACGGCC.CTGGAGGAGGCGCGCGTCTCCGGGAGGGGAACTG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                             184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                  633 GCCATCAGTGAGGACAGTGCTGACGGGGCCCTGGCACT.GGGCCCTGG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCTTTGGGGCTGCACTGTGCNGAGAGTGTCAACAACGAGATGGAACC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euAlaAspTrpTleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCTGACTGGATCCACAGCAGTGGGGGGGGTTGGGGGGGAGTTCACAGCTCTA 583
                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 697)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                           603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5'
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                          BI770566.1 GI:15762144
                                                                                                                                                                                                                                              mRNA sequence.
                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                     697 bp
                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                       linear
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: BI770566 from: 1 to: 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-15\overline{5}-327E-7 \times BI770566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 GGGAGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 294
                                                                                                                                                                                                                                                                                                                                        445 GTCTTTGGGGCTGCACTGTGTTGCTGAGAGTGTCAACAAGGAGATGGAAC 494
                                                                                                                                                                     101 ValPheGlyAlaAlaLeuCys.AlaGluSerValAsnLysGluMetGluP 117
                                                                                                                                                                                                                                              395 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
133 gLeuAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaL 150
                                                                                                                                                                                                                                                                                                                                                                                       67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                  84 sp@luLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 21 High quality sequence stop: 695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://image.llnl.gov
plate: LLAM11526 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /incle="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled lung and spleen; RNA source
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
spleen, and directionally cloned (EcoRV site is destroyed
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MCC Library."

21 a 202 c 248 g 126 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .697
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4.890
97.326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
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REFERENCE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                645 CTGGGCACTCAGTGAGGACAGTTGCTGACGGGAGCCGTGGCACTGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 nTrpAla.SerValArgThrVal.LeuThrGlyAlaValAlaLeuGlyAl 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 TATACGGGGGACGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGAGGGGAA 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 euTyr.GlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAs 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          545 GCTGGCTGACTGGATCCACAGCAGTGGGGGGTTGGGCGGAGTTCACAGCTC 594
      Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Womura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegani,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequence in 'iii '1727-1777', '2000')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409, 685-690 (2001) 5 (bases 1 to 854)
                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                             The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                    FANTOM Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK013244 854 bp mRNA linear HTC 19-JAN-2002 Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810435A13:Bcl2-like 2, full insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone:2810435A13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (2000)
                                                 Quackenbush, J.,
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246 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
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TITLE

TITLE

SOURCE

VERSION

REFERENCE

AUTHORS JOURNAI TITLE AUTHORS

REFERENCE

PUBMED

MEDLINE JOURNAL TITLE

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Align seg 1/1 to: AK013244 from: 1 to: 854
                                                                                                                                                                                                                                     US-09-155-327E-7 x AK013244
                                                                       196 ATGCCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 245
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                        1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rot = 37.5. Second strand cDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN For Schences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax:81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHGKIGPLMGGWGCAGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="matpastpdtralvadevgyklrokgyvcgagpgegpaadplho
AMRAAGDEFETRFRRTFSDLAAOLHVTPGSAQORFTQVSDELFOGGPNWGRLVAFFVF
                                                                                                                                                                                                                                                                                                                                          761.00
5.142
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/db_xref="GI:12850488"
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196. .732
                                                                                                                                                                                                                                                                                                                    98.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="MGD:MGI:1902183"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                               Percent Identity: 95.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 g
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seq_name: gb_est2:BI910270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ValpheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      446 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGCTGACTGGATCCACAGCAGTGGGGGCTGGGTAAGAAGTTCTCAATTG 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 643)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        643 bp mRNA linear EST 16-OCT-2001 603069493F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI910270.1 GI:16173653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: MGC clone distribution information can be
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11548 row: j column: 23
                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: |
Location/Qualifiers
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed): RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note:
                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:5218294"
/clone_lib="NIH_MGC_118"
                                                                                                                                                                                          /tissue_type="leuk
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                      leukocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
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                                                                                                                                                                                                                                                                                                                                DEFINITION
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                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                        ACCESSION
                         COMMENT
                                                                                                                                                                                                                                                                 VERSION
                                                                                                                      REFERENCE
                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                          ORGANISM
                                                                         TITLE
                                                  JOURNAL
                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 490 CACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGCATGGAAC 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGlu.MetGluP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        587 CAAAGCTCGAGTCAGGGAGGATGGAGGAAGAAGCTGAGAAGCTAAAGGAG 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 uTyrGly.....AspGlyAlaLeuGluGluAlaArgArgLeuArgGlu 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 LeuAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGCTGACTGGATCCACAGCAGTGGGGGGCTGG...GAGCTGGAAGCTAT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArg 133
                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est2:BF785386
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                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1__(bases 1 to 815)
                                                                                                                                                                                                                                                              BF785386.1 GI:12090422
                                                                                                                                                                                                                                                                                        5', mRNA sequence.
BF785386
                                                                                                                                                                                                                                                                                                                                     602111728F1 NCI_CGAP_Kid14 Mus
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                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                      house mouse.
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a 184 c 216 g 114 t
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4.831
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                                                                                                                                                                                                                                                                                                                                                                 815 bp
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                                                                                                                                                                                                                                                                                                                                             musculus cDNA clone IMAGE:4239798
                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239
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DEFINITION

SOURCE VERSION

ORGANISM

KEYWORDS

EST

REFERENCE

TITLE

JOURNAL AUTHORS

FEATURES

EST 12-JAN-2001

source

seq_documentation_block:

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alignment_scores:
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                         141 erGlyGlyTrpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGlu 157
                                                                                           347 TTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCA 396
                    397
                                                                                                                                       124 uTrpMetValAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerS 141
                                                                                                                                                                                          298 GCTGAGAGTGTCAACAAGAAATGGAGCCTTG.GTGGGACAAGTGCAGGA 346
                                                                                                                                                                                                                                        108 AlaGluSerValAsnLysGluMetGluProLeuValGlyGlnValGlnG1 124
                                                                                                                                                                                                                                                                                        251 CTAACTGGGGCCGTCTTGTGGCATTCTTGTCTTGGGGC...TGCCTGTGT 297
                                                                                                                                                                                                                                                                                                                                                                                       201 AGCCCAGCAACGCTTCACCCAGGTTTCCGACGAACTTTTCCAAGGGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 CGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTT.GAGACCCGTTTC 150
                                                                                                                                                                                                                                                                                                                    91 roAsnTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCys 107
                                                                                                                                                                                                                                                                                                                                                                                                                74 rAlaGlnGlnArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyp 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 ArgArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlySe 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 roLeuHisGlnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPhe 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 GAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGACC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 nLysGlyTyrValCysGlyAlaGlyProGlyGluGlyProAlaAlaAspp 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 ProAspThrArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGl 24
GTGGGGGCTGGGCGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 3 High quality sequence stop: 650.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 212 c 296 g 141 t
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96.774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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alignment_block:
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                                                                                                                                                                Align seg 1/1 to: BG298789 from: 1 to: 792
                                                                                                                                                                                                              US-09-155-327E-7 x BG298789
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                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                   99 ATGGCGACCCCAGCCTCAACCCCAGACACGGGCTCTAGTGGCTGACTT 148
                                                                                                           1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 GACGGGGCCCTGGCACT.GGGGCCCTGGTAACTGTAGGGGCCCTTTTTGC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 uThrGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544 TAGCACGT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 laSerLys 193
                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://image.llnl.gov
Plate: LLAM10394 row: e column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BG298789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                               174 a
                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="TMAGE:4511215"
/clone="lb4"NH_MGC_94"
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/lab_host="DH10B (phage-resistant)"
/lab_host="Cloned unidirectionally: oligo-dT primed.
Site_2: Sall; Cloned unidirectionally: oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
74 a 201 c 246 g 171 t
                                                                                                                                                                                                                                                                                   99.315
                                                                                                                                                                                                                                                                                                                              733.00
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                                                                                                                                                                                                                                                                                                           5.055
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Percent Identity: 97.945
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101

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seq_name: gb_est1:AW258810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 GCTACACGTGACCCCAGGCTCAGCCCAGCTACCCCAGGTTTCCG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGC.GCTCA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498 TGGCTGACTGGATCCACAGCAGTGGGGGCTGGTAAGAA 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGlu 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValPheClyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW258810

540 bp mRNA linear EST 23-E um74a02.yl Sugano mouse kidney mkia Mus musculus cDNA clone um74a02.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2300906 5' similar to SW:BCLW_MOUSE p70345 APOPTOSIS REGULATOR BCL-W. [2] SW:BCLW_MOUSE;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 540)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person Jackson, M., Pape,D., Harvey,N., Schurk,R., Ritter, E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Watterston,R. and Wilson,R.

Watterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Marra M.WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                           MGI:1009678
                                                                                                                                                                                                                                                                primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                             314 286 1800
314 286 1810
                                                                                                                                                                                                                                        quality sequence stop: 465.
                                                                  /clone_lib="Sugano mouse kidney mkia"
                  /sex="female"
/dev_stage="adult"
                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:2300906"
                                                                                                                                             /strain="C57BL
                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                        Joca L.
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                                                                                                                                                                                                                        on/Qualifiers
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                  SOURCE
                                                KEYWORDS
                                                                        VERSION
                                                                                          ACCESSION
                                                                                                                                                DEFINITION
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                                                EST
                          numan
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SOURCE KEYWORDS VERSION

COMMENT

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alignment_block:
US-09-155-327E-7 x AW258810
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                                                                                                                                                                                                                                                                                   seq_name: gb_est2:BI764428
                                                                                                                                                                                                     seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 eValGlyTyrLysLeuArgGinLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                      134 euAlaAspTrpIleHisSerSerGly 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 TTTGGTGGGACAAGTGCATGATTGGATGGTCGCCTACCTGGAGACACGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTACACGTGACCCCAGGCTCAGCCCAGCCTTCACCCCAGGTTTCCG
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                                                                                                                  603050701F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190792 5',
BI764428.1 GI:15756006
                                             BI764428
                                                                                  mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACCATGTGTG); Site_2: DraIII (CACCATGTG); Ist strand cDNA was primed with an oligo(dT) primer with an oligo(dT) primer 
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                                                                                                                                                                                   758 bp
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                                                                                                                                                                                                     EST 25-SEP-2001
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alignment_block:
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389 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 438
                                                                                                339 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 388
                                                                                                                                                                                                                   289
                                                                                                                                                                                                                                                                                            239 GGGAGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 288
                                                                                                                                                                                                                                                                                                                                                                                            189 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                             67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                             51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                        34 lyGluGlyProAlaAlaAspProLeuHisGinAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                         17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                   GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
Plate: LLAM11477 row: a column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="organ: pooled colon, kidney, stomach; Vector:
pcMV-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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5.205
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/clone="IMAGE:5190792"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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210 CAGCTATGCGTGCTGCAGGGGATGAATTTGAGGAGCGATTCAGACAAGCA 259
                                                                                           169 TGTT.....CCAGAGCCTGCAGGACCAGCATCCTGTGCTTTGCATT 209
                                                                                                                                                                                      119 CGGGCTTTGGTGGAGGATTTTGTGCGGTACAAGTTATGCCAACGTAGTCT 168
                           27 rValCysGlyAlaGlyProGlyGluGlyProAlaAlaAspProLeuHisG 44
                                                                                                                                                                                                                             11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

Seq primer: -40Rp from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EM191403 601 bp mRNA linear EST 11-DEC-200 da 986a10.y1 NICHD XGC Lil Xenopus laevis cDNA clone IMAGE:5129754 5' Similar to SW:AR1_XENLA Q91827 APOPTOSIS REGULATOR R1 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
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                                                                                                                                                                                                                                                                                                                                                                                                          571.50
4.112
84.756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B (phage resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC)
11brary."
125 c 189 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:5129754"
/clone_lib="NICHD XGC Lil"
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seq_name: gb_est1:AA596919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 TTCAGTGAGATCTCCACACAGATCCACGTGACCCCGGCACAGCATATGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 pheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 GACATATCTGGAGACAAACCTGAGAGGCTGGATTCAGAGCAATGGAGGCT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 lalaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyT 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 lyArgLeuValAlaphePheValPheGlyAlaAlaLeuCysAlaGluSer 110
                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA596919 a362 bp mRNA linear EST 19-SEP-1997 vo21f08.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE: 1050567 5' similar to TR:E123735 E123735 R1 MRNA. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                              WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA596919.1 GI:2412354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse
                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
                                                                                                                                                                                                                                                                            MGI:582143
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                                                                                                                                                                                                                                                                                                                                                            314 286 1800
314 286 1810
                                                                                                                                                                                                                                                                                                                                      mouseest@watson.wustl.edu
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
                                                              /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:1050567"
                                                                                                                                                 /strain="C3H"
                                                                                                                                                                     /organism="Mus musculus"
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          330 GGGGCTGCCCTGTGTGCTGAGAGTGTCACAAAG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 GlyAlaAlaLeuCysAlaGluSerValAsnLys 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 TTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 CTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 yTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProGlyGluG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 PheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGlnLeuHi 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 lyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGlyAspGlu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 eupheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePheValPhe 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 sValThrProGlySerAlaGlnGlnArgPheThrGlnValSerAspGluL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPheValGl 19
                                                                                                                                                                                                                                                                                                                          601866718F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106836 5',
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 601)
                                                                                                                                                                                                                                                                                                           mRNA sequence.
                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                    BF204905.1 GI:11098491
                                    Tissue Procurement: ATCC
                                                       Email: cgapbs-r@mail.nih.gov
                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                 numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   characteristic muscle proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rapidly, forming contractile myotubes and producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library constructed by Bob Barstead. The C2CLZ cell line Library constructed by Bob Barstead. The C2CLZ cell line (available from ATCC, catalog # CRL-1772) differentiates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (available from ATCC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           570.00
5.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 c
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Percent Identity: 97.297
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                                                                                                                                                                                                                                                                                                                                                      601 bp
                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                          linear
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seq_name: gb_est2:BE508939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: BF204905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-155-327E-7 x BF204905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                     134 uAlaAsp.TrpIleHisSerSerGlyGly 143
                                                                                                                                    515 CTGGTGGGACAAGTGCAGGAGTGGATGGTGGCTACTGTGAGACGCGGTCT 564
                                                                                                                                                                                   118 LeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgLe 134
                                                                                                                                                                                                                                          465 TCTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCA 514
                                                                                                                                                                                                                                                                   101 alPheGlyAlaAlaLeuCySAlaGluSerValAsnLySGluMetGluPro 117
                                                                                                                                                                                                                                                                                                                                                415 GAACTGTTTGCAAGGGGGCCCCAACTGGGGTTCGCTTGTAGCCTTCTTGG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 TCATGTGATCCCAGGCTCAGCCCAACAACGACTTCACCCAGGTCTCCGAT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 GTTCGAGACCCGCTTCCGGCGTCACCTTCTCTGATCTGGCGGCTCAGCTG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 GGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGAGATGA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 GTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAG
                                                                                                                                                                                                                                                                                                                                                                            85 GluLeuPhe.GlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePheV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 CCAGCCTCGGCCCCAGACCACCAGCGGCTCTGGTGGCAGACATTTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 .HisValThrProGlySerAlaGlnGlnArg.PheThrGlnValSerAsp 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 uPheGluThrargPheArgArg.ThrPheSerAspLeuAlaAlaGlnLeu 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 GlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGlyAspGl 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 lyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProGlyGlu 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ProAlaSerAlaProAsp...ThrArgAlaLeuValAlaAsp.PheValG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                         GGCTGATCTGGATCCAAAGAGAGTGGGGT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: image.lln1.gov
Plate: LLCM987 row: d column: 05
High quality sequence stop: 561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="rhabdomyosarcoma"
/lab_host="DHIOB (phage_resistant)"
/lab_host="DHIOB (phage_resistant)"
/note="Organ: muscle; vector: pOTB7; Site_1: EcoRI;
Site_2: XhOI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the following 5: adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              568.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:4106836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
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alignment_block:
US-09-155-327E-7 x BE508939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: BE508939 from: 1 to: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq_documentation_block:
LOCUS BE508939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
312 ACGATTTGCTGAAGTAGCAGGTAGCCTGTTCCAAGGAGGGGTGAATTNGG 361
                                                                                                                                                                                        262 TTCAGTGAGATCTCCACACAGATCCACGTGACCCCCGGCACAGCATATGC 311
                                                                                                                                                                                                                                                                                  171 TGTT.....CCAGAGCCTGCAGGACCAGCATCCTGTGCTTTGCATT 211
                                                                                                                                                                                                                                                                                                                                                                                121 CGGGCTTTGGTGGAGGATTTTGTGCGGTACAAGTTATGCCAACGTAGTCT 170
                           77 nArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpG 94
                                                                                                                                        61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnG1 77
                                                                                                                                                                                                                                                                                                                                27 rValCysGlyAlaGlyProGlyGluGlyProAlaAlaAspProLeuHisG 44
                                                                                                                                                                                                                                                                                                                                                                                                                             11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

Seq primer: -40Rp from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE508939 612 bp mRNA linear EST 07-AUG-2000 dc14h09.y1 NICHD XGC Lil Xenopus laevis cDNA clone IMAGE:3397121 5' similar to SW:AR1_XENLA 091827 APOPTOSIS REGULATOR R1 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE508939.1 GI:9728714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 612)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Technologies. Note: This is a Xenopus Gene Collection (XGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531.50
3.908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:3397121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 62.651
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161 562	512	144	462	127	412	111	362	94
ArgLeuArgGluGlyAsnTrpAlaSerValArgThrValLeuThrGly 176	TGAATGGATTTCTAACTCTATATGGGGATGGTGCCATAGAAGAAGCCAGG	rpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg			TGTAACAAGGAGATGTCCCCTCTTCTGCCACGGATTCAAGACTGGATGGT	ValAsnLysGluMetGluProLeuValGlyGlnValGlnGluTrpMetVa	GCCGTATAGTTGCATTTTTGGTTTTTGGTGCCGCACTGTGTGCTGAGAAG	
w 01	561	160	511	44	461	127	411	110

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OM of: US-09-155-327E-7 to: N_Geneseq_032802:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: Jun 6, 2002 2:37 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search information block: Query: US-09-155-327E-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query length: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search time (sec): 288.150000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTQ_spool/USQ9155327/runat_06062002_084853_18524/app_query.fasta_1.508
-Q=/cgn2_1/USPTQ_spool/USQ9155327/runat_06062002_084853_18524/app_query.fasta_1.508
-DB=N.Geneseq_032802 -QFMT=fastap -SUFFIX=p2n.rng -GAPOP=12.000
-GAPEXT=0.000 -MMARTCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -YGAPEXT=0.500
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-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -NO_XLPXY -MAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyright (c) 1993-2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              out_format : pfs
                                                                                                                                                                                                                                          4 1.5e-36
1 3.3e-36
2.1e-35
                                                                                                                                                                                                                                                                                  1.5e-36
1.5e-36
                                                                                                                                                                                                                                                                                                                                                                                                                       6.5e-98
1.7e-97
1.7e-97
                                                     1.9e-34
2.3e-33
                                                                                                                                                                                           9.8e-35
                                                                                                                                                                                                                                                                                                          1.5e-36
1.5e-36
                                                                                                                                                                                                                                                                                                                                                            3.6e-37
                                                                                                                                                                                                                                                                                                                                                                                  3.6e-94
1.5e-72
                                                                              2.0e-33
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                                                                                                       1.1e-33
                                                                                                                                           1.1e-33
                                                                                                                                                                                                                                                                                                                                                                        3.0e-72
                2.4e-34
4.1e-34
8.0e-34
                                                                                                                                                                                                                                                                                                                                             6.3e-37
                                                                                                                                                                                                                                                                                                                                    1.0e-36
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                                                                                                                 1.1e-33
                                                                                                                                                                               9.9e-35
                                                                                                                                                                                                        9.0e-35
                                                                                                                                                                                                                   9.0e-35
                                                                                           1.4e - 33
                                                                                                                                                     2.2e-34
                                                                                                                                                                                                                                  2.1e-35
                                                                                                                             .1e-33
                                                                                                                                                                   .3e-34
                                                                                                                                                                                                                                                                                                                                                            588558
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alignment_scores:

alignment_block: US-09-155-327E-7 x AAX25132 Align seg 1/1 to: AAX25132

1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17

from: 1

to: 581

Percent Similarity:

100.000

Percent Identity: 100.000

Length: Gaps:

Quality: 1007.00 Ratio: 5.218

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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:ABL32229 - /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:AAT33694 + /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:AAQ81696 + /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV17638 + /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:ABA73433 - /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:ABA73433 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID AAX25132 standard; DNA; 581 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAX25132
XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          χX
                                                  The present sequence is the human bcl-w gene encoding Bcl-w protein CC (see AAY05530), a pro-survival member of the Bcl-2 family which is CC widely expressed and which is essential for spermatogenesis. The cinvention relates generally to a method of treatment and to an CC animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility, or CC sequences useful for inducing or reducing fertility, or CC animals. Methods are provided for the treatment of infertility, or CC model carries a mutation is at least one allele of the human or CC murine bcl-w gene or in a gene associated with bcl-w. Such animals CC have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined CC by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in a semination or infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility; animal model; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human bcl-w gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09913710-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 32; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY05530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                    protein associated with Bcl-w
Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other:
                                         animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cory S, Gibson L, Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97AU-0009228.
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400.50
386.00
374.50
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754.38
721.37
698.47
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1.1e-33
7.8e-32
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:AAV28334
                                                                                                                                                                                                                                                                                                                                                                                                               documentation_block:
11-FEB-1997;
                                     04-AUG-1998
                                                                       US5789201-A.
                                                                                                                                                                                                                                             ss; bcl-y; bcl-2; cell death pathway; apoptotic;
                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                     Human bcl-y gene.
                                                                                                                                                                                                                                                                                                                        02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            AAV28334 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GGGAGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCTGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProg 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0798897
                                                                                                     /note=
                                                                                                                                                              Location/Qualifiers
1..579
                                                                                                                        /product= bcl-y
                                                                                                                                             /*tag=
                                                                                                   "No stop codon given"
                                                                                                                                           þ
                                                                                                                                                                                                                                               apoptosis; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500
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134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC

150

301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 251 ATGAACTTTTTCAAGGGGGCCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT

350

oLeuValG1yG1nValG1nG1uTrpMetValA1aTyrLeuG1uThrArgL

84

spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100

300

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alignment_scores:
 Percent Similarity:
                                                                                                                               The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.
                                                                                                  Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                               Claim 3; Column 15/16; 27pp; English.
                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding B-cell lymphoma y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-446079/38
                                                                                                                                                                                                                                                                                                                                    growth e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW61392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COCE-) COCENSYS INC.
Quality: 1002.00
Ratio: 5.219
milarity: 99.482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0012201.
97US-0798897.
 Percent Identity: 99.482
                  Gaps:
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alignment_block: US-09-155-327E-7 x AAV28334 Align seg 1/1 to: AAV28334 from: 1 to: 579 201 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 151 101 67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 51 ASpGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 34 51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT 1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 84 67 200 50 100 34 50

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX15946
The present sequence encodes human bcl-y protein (Hbcl-y). The CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and CC proteins may be used to treat conditions associated with a disruption of CC proteins may be used to treat conditions associated with a disruption of CC used in therapies to treat subjects suffering from: strokes, head trauma, CC ushchmer's Disease, neural and muscular degenerative diseases CC Alzhchmer's Disease, neural and muscular degenerative diseases CC (especially multiple sclerosis), myocardial infarction, vitally induced CC (especially multiple sclerosis), myocardial infarction, vitally induced CC cell death, aging, spinal cord injuries and amyotrophic lateral as a CC sclerosis- conditions where cells under go premature cell death as a CC cresult of triggers which may or may not be apparent. They may also be CC used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, and subjects and seven and bcl-y may be used to treat conditions associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 TGGCTGACTGGATCCACAGCAGTGGGGGGGTTGAGGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 GCCATCAGTGAGGACAGTGCTGACGGGGGCCCTGGCACTGGGGGGCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX15946 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding the human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parasite; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                         Disclosure; Columns 15-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Novel bcl-y homologues of the rat and human bcl-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACGGGGACGGGGCCTGGAGGAGGGGGGGGGGACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pAlaServalArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                               modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0012201.
97US-0798897.
97US-0978523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0978523
                                                                                                                                                                                                                                                                                                                                                                                                                       - useful
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888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAX15946 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-155-327E-7 x AAX15946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       percent Similarity:
seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/Na1999.DAT:AAX25133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 GATGAGTTCGAGACCCGCTTCCGGCGCGCACCTTCTCTGATCTGGCGGCCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 ATGAACTTTTTCAAGGGGGCCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                          134
                                                                                                                                                                                                                                                                                                                                                 351
                                                                                                                                                                                                                                                                                                                                                                 117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                      301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AspGlupheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                    167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                          151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                    401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetalaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                        551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                         184 alThrvalGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAGGGCCCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                    TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA
                                                                                                                                                                                                                                                                                      euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                             ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1002.00
5.219
99.482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             percent Identity: 99.482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250
                                                                                                                                                                                                                                                                                                                                                             400
                                                                                                                                                                                                                                                                                                                                                                                                                                        350
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seq_documentation_block:

AAX25133 standard; DNA; 581 BP

05-JUL-1999 (first entry)

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alignment_block:
US-09-155-327E-7 x AAX25133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAX25133 from: 1 to: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see AAY05531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The canimal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male carminals. Methods are provided for the treatment of infertility, or compared to the carminals of the matter of the treatment of infertility, or compared to the carminals of the carminal o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 100.000
                                                                                                      101 GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                            51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                      34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                   51 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                                                                                                                                                               17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                       1 ATGGCGACCCCAGCCTCAACCCCAGACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                          l MetalaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 34; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY05531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9913710-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse bcl-w gene
GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              animal model; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ing, ennancing or convergence infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 1000.00
Ratio: 5.181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cory S, Gibson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97AU-0009228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-AU00764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 98.964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
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XYXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/Na1997.DAT:AAT96577
        Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                              P-PSDB; AAW36047
                                                                          WPI; 1997-489635/45.
                                                                                                       Adams JM,
                                                                                                                                                          27-MAR-1996;
                                                                                                                             (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                          W09735971-A1.
                                                                                                                                                                                      27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                      Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
diagnosis; degenerative disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                           Human bcl-w DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT96577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT96577 standard; DNA; 583 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 ACGAACTITTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                    Cory S,
                                                                                                                                                         96AU-0008965
                                                                                                                                                                                 97WO-AU00199.
                                                                                                                                                                                                                                                                  /product= bcl-w
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                 Gibson LM,
                                                                                             Holmgreen SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500
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8x5555555555555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAT96577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-155-327E-7 x AAT96577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 48; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 GGGAGGGCCCAGCAGCTGACCCGCTGCACCCATGCGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                       117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                       301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 ACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetalaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                     TACGGGGACGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                         TGGTCGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                     pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                               TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                             GGCATCAGTGAGGACAGTGCTGACGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 1000.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1 to: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 98.964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250
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alignment_block:

US-09-155-327E-7 x AAX25134 Align seg 1/1 to: AAX25134

from: 1

to: 583

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/Na1999.DAT:AAX25134
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                                                          alignment_scores:
percent similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX25134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX25134 standard; DNA; 583 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bcl-w gene derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                          identification of molecules and genetic sequences useful for identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are inducing or reducing fertility, or for reducing provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bol-w gene a mutation is at least one allele of the human or murine bol-w gene or in a gene associated with bol-w. Such animals have disorganised or in a gene associated with bol-w. Such animals have disorganised or in a gene associated with bol-w. Such animals have disorganised or in a gene associated with bol-w. Such animals have disorganised or in a gene associated with bol-w. Such animals murine bol-w genetic sequences capable of inducing, enhancing or otherwise featility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animal model;
                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is described as a derivative of the human bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; page 36; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein associated with Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY05532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams J, Cory S, Gibson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1997;
                                                                                                                   Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
                                                                                                                                                                          facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                               infertility.
                                            Quality: 1000.00
                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97AU-0009228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-AU00764.
                             5.181
            Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koentgen F, Print C;
                                                    Length:
                                   Gaps:
                  98.964
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:AAV28333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                            AAV28333 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 GCCATCAGTGAGGACAGTGCTGACGGGGCCCGTGGCACTGGGGGGCCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 TACGGGGACGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 ACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 GCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTCTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTCGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProg 34
                                                                                                                                                                                                                                                                                                                                             (first entry)
 96US-0012201
97US-0798897
                                                97us-0798897
                                                                                                                                                                 /product= bcl-y
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                              /note= "No stop codon
                                                                                                                                                                               /*tag= a
                                                                                                                                                                                                                                                                   cell death pathway; apoptotic; apoptosis; rat.
                                                                                                                                            given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-155-327E-7 x AAV28333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 100.000
151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                      401 TGGCTGACTGGATCCACAGCAGTGGGGGGGTTGGGCGGAGTTCACAGCTCTA 450
                                                           134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                               351 ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT 400
                                                                                                                                                  117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                               101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                           301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                    251 ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                                                                                                                                                                                                                                                                                               201 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                         101 GGGAAGGCCCAGCAGCCGACCGGCTGCACCAAGCCATGCGGGCAGCTGGA
                                                                                                                                                                                                                                                                                           84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe
                                                                                                                                                                                                                                                                                                                                                                                  67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptosic activity and the apoptosis blocking activity, bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression in vivo. Also, antisense const
where prevention of cell death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Column 13/14; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-446079/38.
P-PSDB; AAW61391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            996.00
5.161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Also, antisense constructs can be used in disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 98.446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                             350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
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seq_documentation_block:
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CC especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and apparent. They may also be result of triggers which may not be apparent. They may also be result of triggers which may or may not be apparent. They may also be result of triggers which may or may not be apparent. They may also be result of triggers which may or may not be apparent. They may be cell death, aging, spinal cord injuries and apparent. They may also be result of triggers which may or may not be apparent. They may also be considered period. In contrast, if they act as cell death with a disruption of corpologed cell life span such as cancer (especially maded) period. The contrast, if they act as cell death with culture for cused in this way to develop cell lines which remain viable in culture for contract and myocardial period death stimulators, and extended period. In contrast, if they act as cell death with contract and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX15945 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA encoding the rat bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5883229-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Columns 13-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Novel bcl-y homologues of the rat and human bcl-2 protein \, - useful for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW97391.
                                                                                                                                                                                                                                                                                                                                The present sequence encodes rat bol-y protein (Rbcl-y). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0012201.
97US-0798897.
97US-0978523.
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seq_documentation_block: ID AAT96578 standard

AAT96578 standard; DNA; 581 BP

XEXTXXX

22-APR-1998 (first entry)

AAT96578;

Mouse bcl-w DNA

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alignment_block:
US-09-155-327E-7 x AAX15945
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Ratio: 5.161
Percent Similarity: 100.000
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AAT96578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 579 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GGGAAGGCCCAGCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                          301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 GACGAGTTTGAGACCCGCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                         401
                                                                                                                                                                                                                                                                                                       134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu
                                                                                                                                                                                                                                                                                                                                                                      117 oLeuvalGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ValpheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                   501 GGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGGCCCTGG
                                            551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG
                                                                            184 alThrvalGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                              TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                       TGGCTGACTGGATCCACAGCAGTGGGGGGGCTGGGGGGAGTTCACAGCTCTA
                                                                                                                                                                                                                                                                                                                                                   spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; 198 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.446
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                                                                                                                                                                                                                                                                                                                                                                  400
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alignment_block:
US-09-155-327E-7 x AAT96578
                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                 Align seg 1/1 to: AAT96578 from: 1 to: 581
                                                                                                                                                                                                                                                                                                                               Percent Similarity:
101 GGGAAGGCCCAGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell iransplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate during genetic modification. It can be used to produce recombinant Bcl-w modulators, diagnosis, antibody production or screening of potential
                                                                            34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;
                                                                                                                       51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 50-51; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-489635/45
                                                                                                                                                                                   1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                    1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW36048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09735971-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; degenerative disease; ss.
                                                                                                                                         eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
|||||||||||
                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cory S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96AU-0008965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-AU00199.
                                                                                                                                                                                                                                                                                                                             965.00
5.079
98.446
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1..507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= bcl-w
/note= "q"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibson LM,
                                                                                                                                                                                                                                                                                                                            Percent Identity: 94.819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holmgreen SP;
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CCXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX25135
                  Disclosure; Page 38; 52pp; English.
                                             protein associated with Bcl-w
                                                      An animal model exhibiting reduced levels
                                                                                     P-PSDB; AAY05533.
                                                                                                                                             (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                               WPI; 1999-243890/20.
                                                                                                                                                                           16-SEP-1997;
                                                                                                                                                                                                   16-SEP-1998;
                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                             25-MAR-1999.
                                                                                                                                                                                                                                                    WO9913710-A1
                                                                                                                                                                                                                                                                                                                               Mus sp.
                                                                                                                                                                                                                                                                                                                                                           Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                       animal model;
                                                                                                                                                                                                                                                                                                                                                                                         Mouse bcl-w gene derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501 GCCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 TTTGGTGGGACAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACGGGGACGGGCCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCTGACTGGATCCACAGCAGTGGCGGCTGGGCGGACTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                        Cory S,
                                                                                                                                                                           97AU-0009228.
                                                                                                                                                                                                  98WO-AU00764
                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..507
                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                      Gibson L,
                                                                                                                                                                                                                                                                              מ
                                                                                                                     Koentgen F, Print
                                                  of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400
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The present sequence is described as a derivative of the mouse

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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAX25135 from: 1 to: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-155-327E-7 x AAX25135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bcl-w gene (see AAX25133) and encodes Bcl-w protein (see AAX05533), pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for the identification of molecules and genetic sequences useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 GGGAAGGCCCAGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
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                                                                                                                                                                                                                                                                                                                                                      351 TTTGGTGGGACAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTC 400
                                                                                                                                                                                                                                                                                                                                                                                                            117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGAGITTGAGACCCGITTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                  pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                        TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
GGCATGAGTGAGCACAGTGGTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                     TACGGGGACGGCCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             965.00
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98.446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV41925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID AAV41925 standard; cDNA; 1098 BP.
                                                                                                                                                 alignment_scores:
                                                                        alignment_block:
                              Align seg 1/1 to: AAV41925
                                                          US-09-155-327E-7 x AAV41925
                                                                                                       Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 alThrvalGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1998 (first entry)
                                                                                                                                                                                                                    This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-1997;
21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9831800-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunological disorder; autoimmune disease; anti-infectious agent;
                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feng P,
                                                                                                                                                                                           sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other;
                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                           or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-414099/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AUCK-) AUCKLAND UNISERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW59884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gentz RL, Krissansen GW,
                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0034205.
97US-0034204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US00960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Bcl-like (HAICH29) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                        766.00
5.319
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                                  from: 1 to: 1098
                                                                                                          Percent Identity: 100.000
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                                                                                                                                        Length:
                                                                                                                          Gaps:
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV59630
           02-OCT-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

11-APR-1997
                                                                                                                                                                                                                             Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; inmune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                     06-MAR-1998;
                                                                                                                                                           11-SEP-1998
                                                                                                                                                                                 W09839448-A2
                                                                                                                                                                                                                   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm
                                                                                                                                                                                                                                                                                                                                                19-JAN-1999 (first entry)
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                          Human secreted protein gene 120 clone HGBGZ64.
                                                                                                                                                                                                                                                                                                                                                                                            AAV59630 standard; DNA; 1864 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCTGACTGGATCCACAGCAGTGGGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
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97US-0040162.
97US-0040162.
97US-0040163.
97US-0040333.
97US-0040334.
97US-0040336.
97US-0040331.
                                                                                                               97us-0061060
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    22-AUG-1997
                                                                                                                                                                                                                            08-JUL-1997;
16-JUL-1997;
18-AUG-1997;
22-AUG-1997;
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23-MAY-1997;
23-MAY-1997;
06-JUN-1997;
06-JUN-1997;
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23-MAY-1997;
23-MAY-1997;
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23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
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11-APR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                           13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                            23-MAY-1997;
23-MAY-1997;
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97US-0056862

97US-0056874

97US-0056874

97US-0056875

97US-0056876

97US-0056876

97US-0056877

97US-0056889

97US-0056889

97US-0056888

97US-0056888
                                                                                                                                                                                                                          97US-0043670

97US-0043671

97US-0043671

97US-0047501

97US-0047501

97US-0047581

97US-0047583

97US-0047583

97US-0047583

97US-0047589

97US-0047589

97US-0047593

97US-0047593

97US-0047593

97US-0047597

97US-0047611

97US-0047611

97US-0047613

97US-0047613
                                                                                                                                              97US-0056662.
97US-0056664.
97US-0056845.
                                                                                                                                                                              97US-0056631.
97US-0056632.
97US-0056636.
97US-0056637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0043568.
97US-0043569.
97US-0043576.
97US-0043578.
97US-0043580.
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97US-0043313.
97US-0043314.
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alignment_scores:
                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a nucleic acid molecule designated Gene 120 from the human cDNA clone HGBGZ64 (deposited as clone AFCC 97902 and AFCC 209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human compared to the gene to a human compared to the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic conditions es: AAV59511-v99812; amino acid sequences AAW74731-W75026) conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 186 to plynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                    Align seg 1/1 to: AAV59630
                                                                                                                                                                                                   US-09-155-327E-7 x AAV59630
                                                                                                                                                                                                                                          Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feng P, Ferrie AM, Fischer CL, Flor
Kyaw H, Lafleur DW, Li Y, Moore PA,
Ruben SM, Shi Y, Soppet DR, Young P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 353-354; 721pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bednarik DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                              Sequence 1864 BP; 494 A; 403 C; 506 G; 455 T; 6 other;
                        34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                    17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                             1998-506364/43.
                                                      TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                                                             AAV59511 for described uses).
                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW74848
                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brewer LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0056886.
97US-0056887.
97US-0056888.
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                                                                                                                                                                                                                                                           766.00
5.319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0056892.
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                                                                                                                                                                          from: 1 to: 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carter KC,
                                                                                                                                                                                                                                               Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Florence KA, Greene J
e PA, Ni J, Olsen HS,
                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yu GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Greene JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zeng Z;
                                                              110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endress GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT;ABL32228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGACGTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antirhidammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune system disease; cytosine methylation; antiarteriosclerotic; antianaemic; cytostatic; nooti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune system associated gene SEQ ID NO: 201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL32228 standard; DNA; 6049 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                    WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                           WPI; 2002-130909/17.
                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                          02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCTGACTGGATCCACAGCAGTGGGGGCTGG 442
                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                            Berlin
                                                                                                                                                                                                              ζ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

macular degeneration, arteriosclerosis,

Claim 1; SEQ ID NO 201;

32pp + Sequence Listing;

German.

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seq_documentation_block:
ID AAS00247 standard; DNA; 1236 BP
                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAS00247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SXSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-155-327E-7 x ABL32228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: ABL32228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5351 ATTGGTGGGATAAGTGTAGGAGTGGATGGTGGTTTATTTGGAGACGTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5151 GATGAGTTCGAGATTCGTTTTCGGCGTATTTTTTTTTGATTTGGCGGTTTA 5200
Chimeric - Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5101 GGGAGGGTTTAGTAGTTGATTCGTTGTATTAAGTTATGCGGGGTAGTTGGA 5150
               Chimeric - Corynebacterium diptheriae
                                      Chimeric - Homo sapiens
                                                                                       Human; Bcl-Xl-DTR; apoptosis; cancer; spinal muscular atrophy; ds; diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                   Huntington's disease.
                                                                                                                                                                                                   Bcl-X1-DTR apoptosis-modifying fusion protein, DNA sequence
                                                                                                                                                                                                                                                         31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5001 ATGGCGATTTTAGTTTCGGTTTTAGATATACGGGTTTTGGTGGTAGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6049 BP; 1480 A; 109 C; 1549 G; 2911 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTTTGGGGTTGTATTGTGTGTTGAGAGTGTTAATAAGGAGATGGAATT 5350
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTTGATTGGATTTATAGTAGTGGGGGTTGG 5432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTAGGTTATAAGTTGAGGTAGAAGGGTTATGTTTGTGGAGTTGGTTTCG 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.795
81.250
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alignment_block:

Percent Similarity:

Quality: Ratio:

433.50 2.949 63.090

Percent Identity: 39.914

Sequence 1236 BP;

317 A;

291 C; 343

G; 285 T; 0 other;

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The sequence represents the coding sequence of Bcl-Xl-DTR apoptosis-
CC modifying fusion protein comprising human Bcl-Xl sequence fused via a
CC short linker to diphtheria toxin receptor binding domain (DTR). The
CC functional apoptosis modifying fusion protein is capable of binding a
CC target cell and integrating into or crossing a cellular membrane of the
CC target cell. The apoptosis-modifying fusion protein comprises at least
CC two domains: the DTR domain, which targets the fusion protein to the
CC carget cell and the Bcl-XL domain, which modifies an apoptotic response
CC of the target cell. The fusion protein is useful for modifying
CC target cell and the Bcl-XL domain, which modifies an apoptotic response
CC of the target cell. The fusion protein is useful for modifying
CC target cell and the Bcl-XL domain, which modifies an apoptotic response
CC of the target cell. The fusion protein is useful for reducing
CC inhibiting or enhancing) apoptosis in a target cell, such as neuron,
CC lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or
CC hyper-proliferative cell or an adipocyte. It is also useful for reducing
CC apoptosis in a subject after transient ischaemic neuronal injury,
CC especially spinal cord injury. The fusion protein may be used to treat
CC apoptosis in a subject after transient ischaemic neuronal injury,
CC especially spinal cord injury. The fusion protein may be used to treat
CC various diseases and injury conditions through inhibition or enhancement
CC such as Alzheimer's disease, Huntington's disease, spinal muscular
CC atrophy, stroke episodes and unregulated cell growth as in tumours and
CC atrophy, stroke episodes and unregulated cell growth as in tumours and
CC effectively throughout the body and targeted to selective tissue and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 54-56; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU00219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-2000; 2000WO-US22293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200112661-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE.
(USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-218343/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu X, Collier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0149220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "DTR, diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Linker DNA, linking Bcl-X1 to DTR" 778.1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Bcl-Xl gene from codon 1-233"
760..777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "10x Histidine tag 61..759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Bcl-X1-DTR fusion protein"
/note= "DTR is diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
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seq_documentation_block:
ID AAH43464 standard; cDNA; 702 BP.
XX
AC AAH43464;
XX
DT 04-DEC-2001 (first entry)
XX
DE cDNA clone HP03564 ORF.
XX
XX
XX
XX
Npw38; NpwBP; protein interaction;
XX
XW Npw38; NpwBP; protein network; int
                                                                                                                                                                                                                                                                                                                           seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-155-327E-7 x AAS00247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGCAAG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 AGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 CGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 GACAAGGAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGGTAAACTGGGGTC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 r..... 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 .....ValCysGlyAlaGlyPro 33
     Npw38; NpwBP; protein interaction; reporter function; eukaryotic ccll; localization; protein network; intracellular; primer; amplify; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGAGCTGGTTGACTTTCTCTCCTACAAGCTTTCCCAGAAAGGATA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....ProLeuHisGlnA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnLysGluMetGluProLeuValGlyGlnValGlnGluTrpMetValAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                      yAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaSer 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuArgGlu.....GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 625
                                                                                                                                                                                                                                                                                                                                                                                   CGTGGTTCTGCTGGGCTCACTCTTCAGTCGGAAAGCGTATTCTGCGGCC
                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH43464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: AAS00247
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAH43464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the method of the invention. The method allows detection of interactions between a protein X and a protein Y which has a reporter function in eukaryotic cells, and comprises modifying the localization patterns of X and/or Y, and the localization of Y in the cell is observed using the reporter function. This method is useful for the elucidation of protein networks within the cell. It is also applicable for the discovery of new proteins and low-molecular drugs, by observing their effect on intracellular protein interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of protein-protein interactions for screening compounds capable of modifying the interaction comprises observing intracellular localization of one protein after altering the modification pattern
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase chain reaction; mitochondria; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 702 BP; 165 A; 175 C; 224 G; 138 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the open reading frame of the mitochondrial cDNA clone HP03564. The protein encoded by this sequence was used in the method of the invention. The method allows detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 27-29; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kato S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NISC-) JAPAN SCI & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2000; 2000JP-0073095
24-AUG-2000; 2000JP-0254418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2001; 2001WO-JP01973
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                                                                                                                                                                                                            116 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 165
166 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG
                                                                                                                                                                                                                                                                                                                                                     11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
                                 45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe
                                                                      CAGCAGTTTGGATGCCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAG
                                                                                                                                                                                                                                                                                  CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-590069/66
                                                                                                .....ProLeuHisGlnA 45
                                                                                                                                                                        Quality:
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666 CGTGGTTCTGCTGGGCTCACTC 687

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OM of: US-09-155-327E-7 to: GenEmbl:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: Jun 6, 2002 2:30 PM
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gb_ro:AF096291
gb_pat:AX022531
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Query length: 193
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gb_ro:AF030769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_om:AY005131
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gb_om:AF216205
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                                                                                                                                                                                                                                                                                                                                                                                                  gb_om:AF164517
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8.8e-78 58
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9.9e-64
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.2e-76
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U59746 Mus musculus Bcl-w (bcl
AX022529 Sequence 6 from Patent
AX030817 Sequence 6 from Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF030769 Mus musculus BCL-W ()
AR020779 Sequence 1 from pater
AF096291 Rattus norvegicus Bcl
                                                                                                                                                 X83574 M.musculus bcl-xL mRNA.
U10101 Mus musculus bcl-x long
AF164517 Ovis aries Bcl-x long
AF164517 Ovis aries Bcl-x long
AF054021 Sequence f from patent
AF118504 Sequence 1 from patent
AF124952 Sequence 1 from patent
AF144311 Sequence 39 from patent
AF172594 Sequence 6 from patent
E58777 Screening method of apopt
I52011 Sequence 5 from patent
I Z23115 H.sapiens bcl-xL mRNA.
I Z35049 Mus musculus Bcl-xL mRNA.
I L35049 Mus musculus Bcl-xL mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY005131 Oryctolagus cuniculus
1 U51278 Mus musculus thymus Bcl
1 Ax085490 Sequence 1 from Paten
1 U26645 Gallus gallus bcl-x (bc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : x82462 X.laevis R1 mRNA. 7/199
: ax345130 Sequence 201 from Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AX022531 Sequence 8 from Patent AX030819 Sequence 8 from Patent 1 AX030819 Sequence 10 I AL049829 Human chromosome 10 I AC079885 Rattus norvegicus 1 AC084240 Rattus norvegicus 1 AC084240 Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF216205 Sus scrofa anti-apopto
AJ001203 Sus scrofa mRNA for ar
                                     U72350 Rattus norvegicus Bcl-
BC019307 Homo sapiens, clone
                                                                                                  AB073983 Canis familiaris mRNA
BD006625 A mutagenized rat bcl
         AF060226 Eukaryotic expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_pr:HSU59747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_om:BTU92434
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                                                                                                                                                                                                                             alignment_block:
US-09-155-327E-7 x HSU59747
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                                                                                                                                                                                      Align seg 1/1 to: HSU59747 from: 1 to: 582
                                                                                                                                                                                                                                                                                      Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                            17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                               TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S. bcl-w, a novel member of the bcl-2 family, promotes cell survival oncogene 13 (4), 665-675 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Bc1-w (bc1-w) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U59747.1 GI:1572492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-JUN-1996) Molecular Biology Unit, The Walter an Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                            Quality: 1007.00
Ratio: 5.218
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GAALCAESVNKEMEPLVGQVQEWMYAYLETRLADWTHSSGGWAEFTALYGDGALEEAR
                                                                                                                                                                                                                                                                                                                                                                                                                    RLREGNWASVRTVLTGAVÄLGALVTVGAFFÄSK"
156 c 211 g 111 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="bcl-w"
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2.3e-27
1.7e-27
3.3e-27
1.8e-26
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1 U92434 Bos taurus bcl-2 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ! Z11961 G.domesticus mRNA
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: X82537 R.norvegicus bcl-x
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pr:BC021198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGlupheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 ValPheGlyAlaAlaLeuCysAlaGluScrValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 ACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 GCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTCTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
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              Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
                                                                                                               Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                      DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                          CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Cor
                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC021198 1437 bp mrNA linear PRI 22-JAN-HOMO sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mrNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGC
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                                                                                                                                                                                                             Consortium (LLNL)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAL Plate: 15 Row: k Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14574571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.
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509 g
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Align seg 1/1 to: BC021198 from: 1 to: 1437 Ratio: 5.218 Percent Similarity: 100.000 US-09-155-327E-7 x BC021198 117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134 476 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 525 101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117 376 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 425 326 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 276 GGGAGGCCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA 84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100 226 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50 17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProg 34 1 MetalaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17 ATGAACTITTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 475 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84 Quality: 1007.00 Percent Identity: 100.000 Length: 375 325

526 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC

575

Length:

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seq_name: gb_pr:D87461
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ORIGIN
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          626 TACGGGGACGGGCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAACTGTAGGGGCCTTTTTTGCTAGCAAG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagase, T., Seki, N., Ishikawa, K., Ohira, M., Kawarabayasi, Y., Ohara, O., Tanaka, A., Kotani, H., Miyajima, N. and Nomura, N. Prediction of the coding sequences of unidentified human genes. V The coding sequences of 80 new genes (KLAA0201-KLAA0280) deduced analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human mRNA for KIAA0271 gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens male brain myloblast cell_line:KG-1 cDNA to mrNA, clone_lib:pSPORT 1 clone:HA6752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIAA0271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D87461.1 GI:1944417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohara,O., Nagase,T., Kikuno,R. and Nomura,N. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 3542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 3542)
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177. .758
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GAALCAESVNKEMEPLVGQVQEWMYAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
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/clone="HA6752"
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177. .758
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                            817 c
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alignment_block: US-09-155-327E-7 \times D87461
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                                                                                                                                                                                                                                                seq_name: gb_pat:AR020780
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LOCUS AR020780
FEATURES
                                                                 REFERENCE
                                                                                                                   SOURCE
                                                                                                                                                                 ACCESSION
                                                                                                                                                                                   DEFINITION
                                                                                                                                 KEYWORDS
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                JOURNAL
                                TITLE
                                                 AUTHORS
                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 ATGAACTTTTTCAAGGGGGCCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         477 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                  677 GGCATCAGTGAGGACAGTGCTGACGGGGGCCCTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                       151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCTGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA 626
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Ratio: 5.218
                                                                                                                                                              579 bp
Sequence 2 from patent US 5789201.
                Genes coding for bcl-y a bcl-2 homologue Patent: US 5789201-A 2 04-AUG-1998;
                                                   Guastella,J.
                                                                                                   Unknown
                                                                                                                                                   AR020780.1 GI:3975395
                                                                                                                   Unknown
                                                                                 Unclassified
                                                                 (bases 1 to 579)
Location/Qualifiers
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source

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ACCESSION
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SOURCE
                                                                                            seq_name: gb_ro:MMU59746
                                                                          DEFINITION
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Percent Similarity: 99.482
                                                                                                                                                                              501 GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                     151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                            167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                 451 TACGGGGACGGGCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 GGGAGGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                             TGGCTGACTGGATCCACAGCAGTGGGGGGGGTGGGCGGAGTTCACAGCTCTA 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus Bcl-w (bcl-w) mRNA, complete cds. U59746
                                U59746.1 GI:1572494
                                                                                          MMU59746
house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 1002.00
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154 c 208 g
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                                                                                    582 bp
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                                                                                      mRNA
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                                                                                ROD 29-SEP-1996
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alignment_scores:
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251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                             201 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                 151 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                                                                              101 GGGAAGGCCCAGCCGACCCGACCCAAGCCATGCGGGCTGCTGGA
                            84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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                                                                                                                                                          67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
                                                                                                                                                                                                                                                                                                                                                                               34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT
                                                                                                                                                                                                                                                AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
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Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="bcl-w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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seq_documentation_block:
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17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                        1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 50
                                                               1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes patent: EP 0932674-A 6 04-AUG-1999; AMRAD OPERATIONS PTY LTD (AU)
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Ratio: 5.181
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Gaps:
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
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Sequence 6 from Patent W09735971.
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Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
                                                                                                                                                                                                                                                                        apoptosis-controlling genes
Patent: WO 9735971-A 6 02-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX030817.1 GI:10278311
                                                                                                                                                                                                                                   ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU); GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD
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    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGCATGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACCCCAGGTCTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                        Mus musculus BCL-W (Bcl-W) mRNA, complete cds.
Mus musculus
                                                      AF030769
AF030769.1 GI:2623249
                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 1000.00
Ratio: 5.181
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157 c 210 g 111 t
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alignment_block:
US-09-155-327E-7 x AF030769
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REFERENCE
AUTHORS
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229 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                  17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
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Submitted (21-0CT-1997) Center for Molecular Medicine.
University, 1462 Clifton Road, Atlanta, GA 30322, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 3476)
Ross, A.J. and MacGregor, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 3476)
ROSS,A.J., Waymire,K.G., MOSS,J.E., Parlow,A.F., Russell,L.D. and MacGregor,G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=4
3356. 3364
3356. 3364
/gene="Bcl-w"
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3428. 3441
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1 /gene="Bcl-w"
1 814 c 991 g 875 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Codon_start=1
/product="BCL-W"
/protein_id="ABB6430.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Bcl-w"
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171. .610
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/strain="C57BL/10J"
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Percent Identity:
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VERSION
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LOCUS AR020779
                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_pat:AR020779
                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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                                                                         alignment_block:
US-09-155-327E-7 x AR020779
                                                                                                                                                alignment_scores:
                                                                                                                                                                                                BASE COUNT
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                                                                                                          Ratio: 5.161 Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAACTGTAGGGGCCTTTTTTGCTAGCAAG 757
Sequence 1 from patent US
AR020779
                                                                                                                                                                                                                                   Genes coding for bc1-y a bc1-2 homologue patent: US 5789201-A 1 04-AUG-1998; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                Unknown
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                                                                                                                                    Quality:
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                                                                                                                                                                                                                                                                                                                             Unknown.
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157 c 198 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                           Hamner,S., Skoglosa,Y. and Lindholm,D.
Differential expression of bcl-w and bcl-x messenger RNA in the
developing and adult rat nervous system
Neuroscience 91 (2), 673-684 (1999)
                                                                      Hamner, S., Skoglosa, Y. and Lindholm, D. Direct Submission Submitted (01-0CT-1998) Developmental University, Box 587, BMC, Uppsala 751
                                                                                                                                                                                                                                                                                                      Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus Bcl-w
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                                                                          Neuroscience, Uppsala
23, Sweden
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alignment_block:
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            501
                   167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                      451
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                                                                                                                                                                                     401 TGGCTGACTGGATCCACAGCAGTGGGGGCTGGGCGGAGTTCACAGCTCTA 450
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GGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGGCCCTGG
                                                                                              TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                     OLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                             GTCTTTGGGGCCTGCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
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157 c 200 g 114 t
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/protein_id="AAC64200.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-15\overline{5}-327E-7 \times AX022531
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251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                       151 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA
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                                                                                                             67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
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                      spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe
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Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl-w, belongs to the bcl-2
apoptosis-controlling genes
Patent: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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GAALCAESVNKEMEPLVGQVQDMTVAYLETRLADWIHSSGGMADFTALVGDGALEDAR
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seq_name: gb_pat:AX030819
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                                                                                                                      US-09-155-327E-7 x AX030819
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pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
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A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
patent: WO 9735971-A 8 02-0CT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU); CORY SUZANNE (AU);
GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)
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/translation="MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQ
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GAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGGGGACGGGCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCTGACTGGATCCACAGCAGTGGCGGCTGGGCGGACTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAACTGTAGGGGCCTTTTTTGCTAGCAAG
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 196292)

Hellig, R., Pettl, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Hellig, R., Pettl, J.L., Vico, V., Pelletier, E., Artiguenave, F., Eckenberg, R., Brulls, T., deBerardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Welssenbach, J. Seguencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNS0000B 196292 bp DNA linear PRI 22-MAY-
Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
                     - Web : www.genoscope.cns.fr)
On Jun 3, 2000 this sequence version replaced gi:6138746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL049829.4 GI:8217859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL049829
                                                                                     Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
Center: Genoscope / Centre National de Sequencage
                                                                                                                                        Direct Submission
                                                                                                                                                                Genoscope
                                                                                                                                                                                                    Unpublished
                                                                                                                                                                            (bases 1 to 196292)
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	dbSTS:STS25817 Identified using the e-PCR software (G. Schuler) 128419128543 /note="matching EMBL:R87257	Identified using the e-PCR software (G. Schuler)" 128387128525 /note="matching EMBL:H22648 RHdb:RH53520	MBL:D11677	165	g	dbSTS:STSS5514 Identified using the e-PCR software (G. Schuler)" 9358093808 9360- matching EMBL:AA007328	/HOLE="MACCING EMBL:AA167748 RHdb:RH98727 dbSTS:STS68485 Identified using the e-PCR software (G. Schuler)" 8216482299 /note="matching EMBL:H79035 RHdb:RH78773	E	romosome="14" one="R-124D2" one_lib="RPC" one_lib="RPC" 5978398 ce="matching"	Percentage of bases with a quality value >= 40 : 99 %. Location/Qualifiers rce	59 69 79 99		quality chart :	The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end): R-244E17 Downstream BAC (overlapping the SP6 end): C-2201G16 (AC=AL132855)	Center code: GS Web site: http://www.genoscope.cns.fr/ Contact: SegRef@genoscope.cns.fr
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100	67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84	51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67	34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50 	17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34 	1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17 	US-09-155-327E-7 x CNS0000B Align seg 1/1 to: CNS0000B from: 1 to: 196292	alignment_scores: Quality: 873.50 Ratio: 4.526 Percent Similarity: 48.371 Percent Identity: 47.870 alignment block.	ONTIS: STIS53407 BASE COUNT 50870 a 45673 c 47123 g 52626 t ORIGIN	dbSTS:STS65422 Identified using the e-PCR software (G. Schuler)" STS 194804194903 /note="matching EMBL:N91549 RHdb:RH76320	dbSTS:STS48564 Identified using the e-PCR software (G. Schuler)" 161671161761 STS 161761 /note="matching EMBL:AA452257 RHdb:RH92419	RHdb:RH28671 dbSTS:STS20163 Identified using the e-PCR software (G. Schuler)* STS 138805138926 /note="matching EMBL:H72023 RHdb:RH68657	the e-PCR	GBSTS:STS24710 dbSTS:STS24710 Identified using the e-PCR software (G. Schuler)* STS 138568138647 /note="matching EMBL:M78986	2 930 using the e- 8658 hing EMBL:M7	Identified using the e-PCR software (G. Schuler)* 138462138738 /note="matching FMBL:R50134

FEATURES Source

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HTG 08-NOV-2000

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90076 ATGAACTTTTTCAAGGGGCCCCCAACTGGGGCCCGCCTTGTAGCCTTCTTT 90125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90376 AGTCTCCCCGTCTGGATGGAATTAGATTGAGAGATGCCTGGACTCTGCAC 90425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90476 AGGACAGAATACACACCCAAGGAGTGCCTGCAGGGGAATGTTGTCAGGGA 90525
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                                                                                                                                                                                                                                                                                                    90826 GATATCCCTTCTCCTTCTTCTCTCCTGCTTCCCTTCTCTCCCACAGGC 90875
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90926 TGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGGCCGTG 90975
                                                                                                                                                                                                    90876 GGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTC 90925
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                                                                                                                                                                                                                              146 .GluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArgL 162
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                                                                                                                                                                                                                                                                                                                                             .....Ala 145
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JOURNAL
REFERENCE
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                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Ho,S.-L., Idol,J., Karlins,E., Lee-Lin,S.D., McCloskey,J.C.,
Maduro,O.L., Maduro,V.B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Prasad,A., Snyder,B., Stantripop,S.,
Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W.,
Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D. and Green,E.D.
NISC Mouse Sequencing Initiative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Nov 8, 2000 this sequence version replaced gi:10179358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Norway rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 147800 bases at least Q40 Consensus quality: 148726 bases at least Q30 Consensus quality: 149333 bases at least Q20 Insert size: 145000; agarose-fp Insert size: 150812; sum-of-contigs Quality coverage: 11.76x in Q20 bases; agarose-fp Quality coverage: 11.30x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 151212)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: NIH Intramural Sequencing Center Center code: \ensuremath{\mathsf{NISC}}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                               20441
20541
41010
41110
                                /strain="Brown Norway"
/db_xref="taxon:10116"
                                                                                   /organism="Rattus norvegicus"
                                                                                                           1. .151212
                                                                                                                                   Location/Qualifiers
                                                                                                                                                           20440: contig of 20440 bp in length 20540: gap of unknown length 41009: contig of 20469 bp in length 41109: gap of unknown length 65552: contig of 24443 bp in length 65652: gap of unknown length 110365: contig of 44713 bp in length 110465: gap of unknown length 151212: contig of 40747 bp in length.
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    Summary Statistics
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alignment_scores:
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                                                           74915 TGGCTGACTGGATCCACAACAATGGGGGCTGGGTGGAGTTCACAGCTCTA 74964
                                                                                                                                                                                                                       74865 ATTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCCAGAGACACGCC 74914
                                                                                                                                                                                                                                                                                                       74815 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAGAAAAATAGAGCC 74864
                                                                                                                                                                                                                                                                                                                                                                                    74765 ACGAACTTTTCCAAGGGGGCCCCAACTAGGGCCCATCTTGTGACATTCTTT 74814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74615 GGGAAGGCCCAACAGCCAACCTGATACACCAAGCCATGTGGGCTGCTGGA 74664
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                                                                                                151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                              134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                               117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                            101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                           84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaphePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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110466. .151212
/note="assembly_fragment"
a 30838 c 31177 g 45417 t
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20541. .41009
/note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP31-246H18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....GCTGGCCCCG 74614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75015 GGCATCAGTGAGGACAATACTGACTGGGGCTGTGACACTGGGGACCCTGA 75064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75065 TAACTGTAAGGGCCTTTTTTACTAACAAG 75093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Dietrich, N.L., Gupta, J., Ho, S.-L., Idol, J., Lee-Lin, S.-O., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Snyder, B., Stantripop, S., Thomas, J.W., Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tran, J.T., Tsurgeon, C. Vogt, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Blg Dye; 100% of reads
Assembly program: Phrap; version 0,990319
Consensus quality: 179798 bases at least Q40
Consensus quality: 180132 bases at least Q30
Consensus quality: 180274 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 160000; pulse-field-gel
Insert size: 180982; sum-of-contigs
Quality coverage: 15.02x in Q20 bases; pulse-field-gel
Quality coverage: 11.45x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC084240.1 GI:10864175
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39604
85793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: nisc_mouse@nhgri.nih.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: rl
Center clone name: 103L21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.nisc.nih.gov
Location/Qualifiers
         5430: contig of 5430 bp in length
5530: gap of unknown length
39503: contig of 33973 bp in length
39603: gap of unknown length
85792: contig of 46189 bp in length
85892: gap of unknown length
181282: contig of 95390 bp in length.
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alignment_block:
US-09-155-327E-7 x AC084240
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ORIGIN
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                                                                                                                                                                                                    50039
                                                                                                                                                                                                                                                                                                                                       49939
                                                                                                                                  50089 ATTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCCAGAGACACGCC 50138
                                                                                                                                                                  117
               151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                misc_feature
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                                                                                                                                                                                                                                                                   67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                          51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                               euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
|||||||||||||||||
|TGGCTGACTGGATCCACAACAATGGGGGCTGGGTGGAGTTCACAGCTCTA 50188
                                                                                                                                                  OLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
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Quality:
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39604. .85792
39604. "assembly_fragment"
85893. .181282
/note="assembly_fragment"
a 36290 c 37296 g 56560 t
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| Strain="Brown Norway"
| /db_xref="taxon:10116"
| /chromosome="4"
| /clone="RP31-103L21"
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clone_end:SP6
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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4: /cgn2_6/ptodata/1/
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US-09-277-020-3
US-09-373-743-1
US-09-374-37-30-3
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PCT-US-94-07089-1
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Sequence 19, Appl
Sequence 14, Appl
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Sequence 14, Appl
Sequence 4, Appli
Sequence 2, Appli
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Sequence 7, Appli
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          ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                         PRIOR APPLICATION DATA:
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CITY: Wa
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COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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1100 New York Avenue, N.W., Suite 600
202-371-2540
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                                            1483.0140002
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; Patent No. 5789201
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                   COMPUTER READABLE FORM:
                                                                                                                  NUMBER OF SEQUENCES: 5
                                                                                                                                               APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y,
TITLE OF INVENTION: Homologue
                                                                                                                                                                           APPLICANT:
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LENGTH: 579 base pairs
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
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Sequence 2, Application US/08978523 Patent No. 5883229

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; MOLECULE TYPE: cDNA US-08-978-523-2
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APPLICANT: Guaste
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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TELEPHONE: 202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: STERNE, NEGOTIAN, --- STREET: 1100 New York Avenue, N.W., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: February 11,
CLASSIFICATION: 424
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                                                                                                                                                                                NAME: Esmond, Robert W. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/798,897
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361 caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc 420
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                                                                                                                     241 caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
248 ccgacgaacttttccaagggggccctaactggggccgtcttgtggcattctttgtctttg 307
                                   454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
                                                      188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
                                                                                                    394 AGCAAGCGCTGAGGGAGGCGAGGCGACTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453
                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                       128 accaagccatgcgggctgctggagacgagtttgagacccgttttccgccgcaccttctctg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: NO. 5646008thrup, Thomas E. REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 GGGGCCCTGGTAACTGTAGGGGCCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 19930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGGCCGTGGCACTG 540
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CITY: Chicago
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                                                                                                                                                                                         Score 134.6; DB 1; Length 926; Pred. No. 8.7e-28;
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                                                                                                                                                     TELEFAX: (512) 474-75 INFORMATION FOR SEQ ID NO:
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                                                     FEATURE:
                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: AR TELECOMMUNICATION INFORMATION: (512) 418-3000
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Texa COUNTRY: Un ZIP: 77210
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                               NAME/KEY:
                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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(512) 474-7577
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                                                                    Linear
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Query Match Best Local Similarity

23.1%; 58.3%;

Score 134.6; DB 2 Pred. No. 8.7e-28; 0; Mismatches 169

DB 2; 169;

Length 926;

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Matches 236;

Conservative

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NAME/KEY:
CDS
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US-08-481-739-1
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                                                                                                                                      REFERENCE/DOCKET NUMBER: RP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)277-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ. ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: June, Carl H. and Thompson, Craig B.
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIV.
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: DECORIT, Giulio A.
15
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   488 gggaggggaactgggcatcagtgaggacagtgctgacgggggccg 532
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                                                                                                                  SEQUENCE CHARACTERISTICS:
FEATURE:
                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                       LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                        TOPOLOGY:
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                    DNA (genomic)
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Patent No. 6172216
                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nicholaf, Brian J.
APPLICANT: Nicholaf, Brian J.
APPLICANT: Zhang, QingQing
APPLICANT: Zhang, QingQing
APPLICANT: Zhang, OingQing
APPLICANT: Zhang, OingQing
                                                                         Best Local Similarity 58.3%; Matches 236; Conservative
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CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                            PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: ISPH-0324
                                                                                                                                                                                                                                                                                                                                      LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (135)..(836)
                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                            Score 134.6; DB 4
Pred. No. 8.7e-28;
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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 39
LENGTH: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
TITLE OF INVENTION: of mRNA Processing
FILE REFERENCE: ISPH-0339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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ORGANISM: Homo sapiens
634 cagcttggatggccacttacctgaatgaccacctagagccttggatccaggagaacggcg 693
                                                                                              368 aggattggatggtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
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Pred. No. 8.7e-28;
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Best Local Similarity
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SEQ ID NO 1
LENGTH: 926
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EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Antisense Modulation of bcl-x Expression FILE REFERENCE: ISPH-0368
CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nickoloff, Brian J. APPLICANT: Zhang, QingQing
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APPLICANT: Dean, Nicholas M.
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754 aggaacgcttcaaccgctggttcctgacgggcatgactgtggccg 798
                               488 999aggggaactgggcatcagtgaggacagtgctgacggggggccg 532
                                                                                      694 gctgggatacttttgtggaactctatgggaacaatgcagcagccgagagccgaaagggcc
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Pred. No. 8.7e-28;
0; Mismatches 169; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                   394 AGCAAGCGCTGAGGGAGGCGAGGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                   128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
                                                                                                                                                                                                                                                                                                                                          188 acctggccgctcagctacacgtgaccccaggctcagcccaggcaacgcttcacccaggttt 247
                                                                                                                                                                                                                                                                                                                       454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
                                                                                                                                                                                   308 gggctgcctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtgc 367
                                                                                                                                                                                                                                         514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573
694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCCGAGAGCCGAAAGGGCC 753
                                     428 gctgggcggagttcacagctctatacggggacggggccctggaggaggcacggcgtctgc 487
                                                                             634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 693
                                                                                                                 368 aggattggatggtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
                                                                                                                                                           574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633
                                                                                                                                                                                                                                                                 248 ccgacgtacttttccaagggggccctaactggggccgtcttgtggcattctttgtctttg 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Thompson, Craig B.B.
Boise, Lawrence H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,511A
EPILNG DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: ARCD:179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 37,642
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135..836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 134.6; DB 4; Length 926; pred. No. 8.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compation operating SYSTEM: PC-DC CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/08
FILING DATE: 22 JUNE 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                     128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: CONCUI
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                                                                                                                                                                454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
                                                                                                                                                                                   188 acctggccgctcagctacacgtgaccccaggctcagcccaggcaacgcttcacccaggttt 247
                                                                                                                                                                                                                                394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453
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                                                                                                  514 TGAATGAACTCTTCCCGGATGGGGTAAACTGGGGTCGCATTGTGGCCCTTTTCTCCTTCG 573
                                                                                                                       248 ccgaccttttccaagggggccctaactggggccgtcttgtggcattctttgtctttg 307
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368 aggattggatggtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
                                    574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633
                                                              308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtgc 367
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                                                                                                                                                                                                                                                                                                     236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   926 base pairs
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SYSTEM: PC-DOS/MS-DOS, ASCII
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arnold,
                                                                                                                                                                                                                                                                                                                                                                                                  135..836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                     23.1%;
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                                                                                                                                                                                                                                                                                                       0; Mismatches 169; Indels
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US-08-465-485A-20
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Sequence 20, App. ...
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                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (408) 436-2070
244 GCGGGGCCTGCGCTCAGCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGGCCAAGCCGGC 303
                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                    91 gctggccctggggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctgga 150
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                                                                                                                                                                            NAME/KEY:
                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Regulation of bcl-2 Gene Expression NUMBER OF SEQUENCES: 29
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                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0'
FILING DATE: 22-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 21-FEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488 gggagggaactgggcatcagtgaggacagtgctgacggggggccg 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                213;
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1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                         single
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                                                                                                                                                                                                                                                                                                                                      436-2075
                                                                                  20.9%; Score 121.8; DB 2; Length 717; 58.4%; Pred. No. 2.5e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                     34,600
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US-09-080-285-20
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Patent No. 6
                               TELEFAX: (408) 436-20 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
                                                                               REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
                                                                                                                                                FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                FILING DATE: 21-FEB-PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER: US 07/840,716
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/465,485
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
                                                                   TELEPHONE:
                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1755 S. CITY: Arlington STATE: Virginia
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                                                   (408) 436-2070
(408) 436-2075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: P.C.
1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                   05-JUN-1995
                                                                                                                                                                                                                 21-FEB-1992
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                                                                                                                                                                                   US 07/288,692
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Best Local Similarity 50...
213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US, patent No. 5834309 Patent No. 5834309 5710045
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,448
FILING DATE: 22-JUN-1993
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484
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LOCATION:
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                                                                                                                                                                                                                                              STREET:
CITY: F
STATE:
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ZIP: 77210
                                                      CLASSIFICATION: 514
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                                                                       FILING DATE:
                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                    Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08470670A
                                                                                                                                                                                                                                                  Texas
                                                                                                                                                                                                                                                                                   E: Arnold, White & Durkee P.O. Box 4433
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Search completed: June Job time: 4723 sec

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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             483 GCGACCTCACCTCCCAGCTCCACATCACCCCTGGCACGGCGTACCAGAGCTTTGAGCAGG 542
                                                                                                                                                                                                                                                                                                                  185 ctgacctggccgctcagctacacgtgaccccaggctcagcccaggcaacgcttcacccagg 244
                                                                                                                                                                                                                                                                                                                                                                    423 TGAGGCAGGCGCTGAGAGATGCGGGGGATGAGTTTGAGCTGAGGTACCGGAGGGCTTTCA 482
                                                                                                                                                                                                                                                                                                                                                                                        125 tgcaccaagccatgcgggctgctggagacgagtttgagacccgttttccgccgcaccttct 184
                                                                                                                                                                                                                     543 TAGTGAATGAACTCTTCCATGATGGTGTGAACTGGGGGCGCGTTGGTGGCTTTCTTCTCCT 602
                                                                                                                                                                                                                                        245 tttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattctttgtct 304
                                                                     663 TTGTGTCTTGGATGACCACGTACTTGACCGACCATCTAGATCCCTGGATCCAGGAGAATG 722
                                                                                                                                             603 TCGGAGGGGCTTTGTGCGTGGAGAGCGTGGACAAGGAGATGCGGGTACTGGTGGGACGCA 662
                                                                                                                                                                  305 ttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaag 364
723 GCGGCTGGG 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            192;
                                  gcggctggg 433
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DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	214 6	233.6	246.8		254 2	277.4	286.8	325.4	366.8	411.6	417	429.8	430.6	445	495.6	496.2	578.8	578.8	Score	
	36.9	40.1	42.4		43 7	47.7	49.3	55.9	63.0	70.7	71.6	73.8	74.0	76.5	85.2	85.3	99.5	99.5	Query Match	æ
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21.0 20.9 20.8 20.7 20.7	22.5 22.5 22.5 21.0 21.8 21.8 21.8	22.5.17	35.2 32.4 31.5 31.3
690 513 456 571 657	965 974 913 862 818 890 890 836	549 548 548 687 700 700	601 612 447 431
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BJ060637 BM363392 AZ537061 BJ041701 BJ062464	BM457276 BB250036 BB2244406 BG244406 BG973530 BG824757 AL537680 BG186671 BG186671 BG1822971	AQ532175 AQ665088 BB188975 AL632408 BE293685 AQ401160 BG831301 BE870269	BM191403 BE508939 BB851239 AW048567 AW159063
BJ06083/ BM363392 BS320054B AZ537061 AST-2P015 BJ041701 BJ041701 BJ062464 BJ062464	'by	AQ533175 RPC1-11-3 AQ65508B HS_5340_B BE188975 db65205.x AL6332408 AL632408 BE293685 601186941 AQ401160 HS_5062_A BG831301 602766132 BE870259 601447403 B1457116 603185360	daj86a10 dc14h09. B851239 I-M-BH1- a50h02.x

ALIGNMENTS

JOURNAL MEDLINE	TITLE	MEDLINE PUBMED REFERENCE AUTHORS	TITLE JOURNAL	PUBMED REFERENCE AUTHORS	REFERENCE AUTHORS TITLE JOURNAL MEDLINE	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 AK015644 LOCUS DEFINITION
Genome Res. 10 (11), 1757-1771 (2000) 20530913	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Kashiwagi, K., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format RIKEN integrated sequence analysis (RISA) system-384-format	20499374 11042159 3 (Sites) 3 (Sites) 3 (Sites) 3 (Sites) 3 (Sites) 3 (Sites) 4 (Sites) 4 (Sites) 5 (Sites) 7 (Sites) 7 (Sites) 8 (Sites) 9 (Sites) 1 (Sites) 1 (Sites) 1 (Sites) 1 (Sites) 2 (Sites) 3 (Sites) 3 (Sites) 3 (Sites) 3 (Sites) 3 (Sites) 3 (Sites) 4 (Sites) 5 (Sites) 6 (Sites) 7 (Sites) 7 (Sites) 8 (Sites) 8 (Sites) 9 (Sites	Normalization and subtraction of cap-trapped selected character prepare full-length cDNA libraries for rapid discovery of new genes genome Res. 10 (10), 1617-1630 (2000)	10349636 2 (sites) 2 (carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., 1toh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	l (sites) Carninci, P. and Hayashizaki, Y. Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	ARG15644 ARG15644.1 GI:12854052 HTC: CAP trapper. Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:4930488D08.	AKO15644 1949 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930488D08:Bcl2-like 2, full insert sequence.

Query Match

Local

Similarity

99.5%;

Score 578.8; DB 11 Pred. No. 4.6e-132;

DB 11;

Length 1949;

0,

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BASE COUNT
ORIGIN
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                                                                          RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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/db_xref="G:1284053"
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BIBGONWA SYLDETRIADWIHSSGGWAEFTALYGDGALEEAR
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132. .713
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/clone_lib="RIKEN_full-length enriched mouse cDNA library"
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                          Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                    3487 bp mRNA linear HTC 19-JA Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200009L24:Bcl2-like 2, full insert common-AK004680
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Mammalia; Eutheria;
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5 (bases 1 to 3487)
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209. .790
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/note="Bcl2-like 2
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                Homo sapiens
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AMRAAGDEFETRERRTSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVQDWMYAYLETRLADWIHSSGGWAEFTALVGDGALEEAR
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541 ggggccctggtaactgtaggggccttttttgctagcaagtga 582
                                                                                       481
                                                                                                                  554 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGAC-GGGCCCTGGAGGAGGCGCGG
                                                                                                                                                                                             434
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                                                            cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg 540
                                                                                                                                         agt9gc9gct9ggcggagttcacagctctatacggggacgggggccctggaggaggcacgg
                                         CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGGCCGTGGCACT-
                                                                                                                                                                                                                                                                           GTCTTTGGGGCTGCACTGTGTGCNGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
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                                                                                                                                                                                                                                                                                                                                                      CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGGCCGCCTTGTAGCCTTCTTT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No s1 sequence available.
This clone (DKFZp/61D0816) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140: Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
Contact: Ansorge W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 804)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email S. Wiemann@dkfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany
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/clone_lib="761 (synonym: hamy2)"
/tissue_type="amyydala"
/dev_stage="adult"
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217 c 294 g 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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142 t 1 others
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TITLE
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241 caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt 300
                                                                                                                             264 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 323
                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                       144 ATGGCGACCCCAGCCTCGGCCCCAGACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 203
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                                                                                                                                                                                                                                                                                                                              1 atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
                                           TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC
                                                                      AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                    528;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. Plate: LLCM800 row: p column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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//note="Organ: lung; Vector: pOTBF; Site_1: XhoI; Site_2: FOORI; cDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3944307"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Stratagene) and Superscript II RT (Life Technologies)."
284 c 386 g 170 t
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90.7%;
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Pred. No. 1.1e-111;
0; Mismatches 54;
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481. cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
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602111728F1 NCI_CGAP_Kidl4 Mus musculus cDNA clone IMAGE:4239798
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 3 High quality sequence stop: 650.
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                                       Similarity
                                                                                                                                       /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone_"IMAGE:4239798"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pcMv-SPORT6; Site_1: NotI;
/note="Organ: kidney; Vector: pcMy-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
a 212 c 296 g 141 t
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                                                                                                                                                                                                                                                                                                                              /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                       76.5%;
96.5%;
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                                                             DB 10; Length 815;
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                                                                           FEATURES
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                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 ggctgctggagacgagtttgagacccgtttccgccgcaccttctctgacctggccgctca 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 ccaagggggccctaactggggccgtcttgtggcattctttgtcttttggggctgccctgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 tgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtgcaggattggatggt 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 CCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCT---TGTCTTGGGGCCTGCCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGGCCGACCCGACCCAAGCCATGCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI770566
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI770566.1 GI:15762144
                                                                                               High quality sequence start: 21 High quality sequence stop: 695.
                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM11526 row: k column: 15
                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 697)
                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 ATGGCGACCCCAGCCTCGGCCCCAGACACGCGCCTCTGGTGGCAGACTTTGTAGGTTAT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 aggctgaggcagaagggttatgtctgtggagctggccctgggggaaggcccagccgac 120
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                                                                                                                                                                                                                                                                                                                                                                                             cactgggggccct 548
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                                                                                                                                                                     enriched library, clone:2810435A13:Bc12-like 2, full insert
                                                                                                                                                                                          AK013244 854 bp mRNA linear HTC 19-JAN-2007 Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
clone:2810435A13
                                   Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA,
                                                                                                                                                          sequence.
                                                                      HTC; CAP trapper
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Similarity 92.0%;
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          lib:RIKEN full-length enriched mouse cDNA library
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                                                                                                                                  Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GACAGAGAGAGATCCAAGACCTCTTTTTTTTTTTTTTYNY 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to
with XhoT and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
                                                                                           of sequence [5'
                                                                                                       Rot = 37.5. Second strand cDNA was prepared with the primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222; Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-2000) roshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format Senome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new g Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
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                                                       602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511215
BG298789.1 GI:13063794
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                            BG298789
                                          mRNA sequence.
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/db_xref="GI:12850488"
/db_xref="GI:12850488"
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GAALCAESVNKEMEPLYGQVQDWMVAYLETRLADWIHSSGGWVRSSQLLLSASLYKVG
LHGKIGPLMGGWGCAGRG"
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/note="BCl2-like 2
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/db_xref="MGD:MGI:1902183"
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518 AGTGGGGGCTGGTAAGA 534
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="retina"
/lab_host="PH10B (phage-resistant)"
/lab_host="PH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Notigned and constructed by Life Technologies.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Note: this is a NIH_MGC Library."
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Pred. No. 2.4e-92;
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                                                                                                                172 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCCAGCCGCCGAC 231
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Similarity 98.8%;
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 465
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
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/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
/note="Organ: kidney; Vector: primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Sugano mouse kidney mkia"
/sex="female"
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/clone="IMAGE:2300906"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs=r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11548 row: j column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 643.
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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     1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
                                                                                                                   /clone="NHH_MGC_118"
/clone=lib="NHH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="PH10B"
/lab_host="Wector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source leukocytes from annomymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range
                                                                                                              cloning). /
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Query Match

Best Local Similarity

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Score 366.8; DB 10; Pred. No. 5e-80;

Length 643;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vo21f08.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1050567 5' similar to TR:E123735 E123735 R1 MRNA. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                      Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
                                                                                                                                                                                                                                                         WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                               Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                    Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA596919.1 GI:2412354
                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nouse mouse
                                                                                                                                                                                                         Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 362)
                                                                                                            primer: -28m13 rev2 ET from Amersham
                                                                                      quality sequence stop: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
/db_xref="taxon:10090"
              /strain="C3H"
                                /organism="Mus musculus"
                                                                      ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                             603050701F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190792 5',
                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                             Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 758)
                                                                                                                                                                                                                                                                                   BI764428.1 GI:15756006
                                                                                                                                                                                                                                                                                                                  mRNA sequence.
             DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                      National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                          Unpublished (1999)
                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3/]; double-stranded CDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            characteristic muscle proteins.
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/cell_line="C2C12"
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98.2%;
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Pred. No. 6.6e-70;
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Ishii Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306;
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                Eukaryota;
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/clone="IMAGE:5190792"
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90.5%;
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Pred. No. 2.6e-60;
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                                                                                                                                                                                                              Sciurognathi; Muridae; Murinae; Mus.
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441 GTCTTTGGGGCTGCC 455
                                                                                                                                                                                       source
                             301 gtctttggggctgcc 315
                                                                                                                       241 caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt 300
                                                                                           384 CAGGTTT-CGACGAACTTTT-CAAGGGGGCCCTAACTGGGGCCGTC-TGTGGCATTCTTT
                                                                                                                                                                                                                                                                                              264 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                  204 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC
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                                                                                                                                                                                                                                                                                                                            ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y. and Hayashizaki,Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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/clone="6370030007"
/clone_115="RIKEEN full-length enriched, B16 F10Y cells"
/cell_type="B16 F10Y cells"
154 c 137 g 85 t
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/strain="C57BL/6J"
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RESULT 1
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Best Local :
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                                                                                                                                                                                                                                          366
                                                                                                                                                                                                                                                                        241 caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattctt 299
                                                                                                                                                                                                                                                                                                                                                                                               246 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCCGCTTCCGGCGCACC 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 aggctgaggcagaagggttatgtctgtggagctggccctggggaaggcccagccgccgac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccqctqcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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602624059F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4748943 5',
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BF204905 601 bp mkNA linear Est of the first column of the first c
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/lab_host="DH10B (Tl phage=reststant);
/note="Organ: skin; Vector: pcMV-SPORT6; Site_1: Not1;
/note="Organ: skin; Vector: pcMV-SPORT6; Site_1: Not2; 
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/db_xref="taxon:9606"
/clone="IMAGE:4748943"
/clone_lib="NCI_CGAP_Skn4"
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90.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      524 CAAGTGCAGGAGTGGATGGTGGCTACTGTGAGACGCGGTCTGGCTGATCTGGATCCAAAG 583
                                                        361 caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc 420
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1 (bases 1 to 601)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
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Plate: LLCM987 row: d column: 05
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/note="organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="organ: muscle; Vector: pOTB
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Search completed: June 6, 2002, 11:24:34 Job time: 5590 sec

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Maximum Match 100%
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ALIGNMENTS

RESULT MMU59746 LOCUS KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION REFERENCE REFERENCE VERSION TITLE JOURNAL JOURNAL TITLE AUTHORS AUTHORS MEDLINE Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 582)
1 (bases 1 to 582)
Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
bcl-w, a novel member of the bcl-2 family, promotes cell survival
Oncogene 13 (4), 665-675 (1996)
96358615 Mus musculus Bcl-w (bcl-w) mRNA, complete cds. Direct Submission Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Gibson, L., Holmgreen, S.P., Huang, D.C.S., Cory,S. house mouse. U59746.1 GI:1572494 (bases 1 to 582) Bernard, O., ROD 29-SEP-1996 Adams, J.M. and

Result No.

Score

Match Length DB

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                     cytctycgggaggggaactgggcatcagtgaggacagtgctgacggggggcgtggcactg
                                                                                                                                                     AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCCTGGAGGAGGCACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Bc1-w"
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RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
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                    ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgttttccgccgcacc
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CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGAC 298
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Submitted (21-OCT-1997) Center
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Ross, A.J. and MacGregor, G.R.
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3356. 3364
/gene="Bcl-w"
/note="mRNA destabilization e
3428. 3441
/gene="Bcl-w"
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/strain="C57BL/10J"
/db_xref="taxon:10090"
/chromosome="14"
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atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
                                                            ATGCCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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                                                                                                                                                                                                                                                                                                     Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes
Patent: WO 9735971-A 8 02-CCT-1997;
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Sequence 8 from Patent W09735971.
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  Conservative
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GAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR
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                                                                                                Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala University, Box 587, BMC, Uppsala 751 23, Sweden
                                                                                                                            Direct Submission
                                                                                                                                   2 (bases 1 to 582)
Hamner,S., Skoglosa,Y. and Lindholm,D.
                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
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RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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1 (bases 1 to 582)
1 (bases 1 to 582)
2 (bases, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival 96358615
96358615
2 (bases 1 LO July Gibson, L., Holmgreen, S.P., Cory, S.
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/db_xref="taxon:9606"
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/protein_id="AAB09055.1"
/db_xref="GI:1572493"
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241 caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt 300
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                                                                                                                                    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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                                      TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCCAACAACGCTTCACC 416
                                                                                                                CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 356
                                                             ttetetgacetggeegeteagetacaegtgaceceaggeteageceageaaegetteace 240
                                                                                                                                                                                              AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC 296
                                                                                                                                                                                                                    aggctgaggcagaagggttatgtctgtggagctggccctgggggaaggcccagccgccgac 120
                                                                                                                                                                                                                                                                         ATGGCGACCCCAGCCTCGGCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 236
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Nagase, T., Seki, N., Ishikawa, K., Ohira, M., Kawarabayasi, Y., Ohara, O., Tanaka, A., Kotani, H., Miyajima, N. and Nomura, N. Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (E-mail:dhainfo@kazusa.or.jp, Tel:+81-438-52-3913)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohara,O., Nagase,T., Kikuno,R. and Nomura,N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="Baa19666.1"
//db_xref="GI:1944418"
//db_xref="GI:1944418"
//tzanslation="Matpasapdtralvadevgyklrokgyvcgagpgegpaadplho
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gaalcarsvnkemeplvgoyoewmvayletrladwihssggwabftalygdgaleear
glregnwasvrtvltgavalgalytvgaffask"
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177...7
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177. .7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_line="KG-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
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Вb Qy В Qγ В

61 aggctgaggcagaagggttatgtctgtggagctggccctgggggaaggcccagccggcc 120

AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC

Matches 543; Query Match

LOCAL

Similarity

89.3%; 93.3%;

Score 519.6; DB Pred. No. 4e-111; Mismatches

DB 6;

39;

Indels Length 583;

0

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0,

Conservative

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Patent: EP 0932674-A 6 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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Sequence 6 from Patent EP0932674.
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157 c 210 g 111 t
                                                                                                                                                                   /note="unnamed protein product"
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aggctgaggcagaagggttatgtctgtggagctggccctggggaaggcccagccgccgac 120
                                                           atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
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Sequence 6 from Patent WO9735971.
AX030817
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                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes patent: WO 9735971-A 6 02-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                          ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unclassified
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                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                /organism="unidentified"
                                                                                                                    89.3%;
93.3%;
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                                                                                                                    Score 519.6;
Pred. No. 4e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC021198 1437 bp mRNA linear PRI 22-JAN-
Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,
                                                                                                                                                                                                                                                                                                                                                                                           submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                    CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                        Contact:

nisc_mgc@nhgri.nih.gov

Shevchenko,Y., Wetherby,K.D., Bekstrom-Sternberg,S.M.,

Shevchenko,Y., Wetherby,K.D., Bekstrom-Sternberg,S.M.,

Benjamin,B., Blakesley,R.M., Bouffard,G.G., Brinkley,C., Brooks,S.,

Benjamin,B., Blakesley,R.M., Bouffard,G.G., Karlins,E., Legaspi,R.,

Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,

Lim,M., Maduro,Q.L., Mastiello,C., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,

Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                   Web site:
                                                                                                                                                                                  Gaithersburg, Maryland;
Zhang, L.-H. and Green, E.D.
                   Tiongson, E.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 1437)
                                                                                                                                                                     http://www.nisc.nih.gov/
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716 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA
                                     541 9999ccct99taact9tag999gccttttttgctagcaagtga 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC 295
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                                                                                                                                                                                                 cytct9c9g9ag9g9aact9g9catcagt9ag9acagt9ct9ac9g9g9gccgtg9cactg 540
                                                                                                                                                   CGTCTGCGGGAAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGGCCGTGGCACTG
                                                                                                                                                                                                                                                                                                           AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCCTGGAGGAGGCGCGG
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14574571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303
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/product="BCL2-like 2"

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/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/db_xref="LocusID:599"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Vector: porm7"
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ACCESSION VERSION

AC079885

AC079885.2 GI:11120768

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ACCESSION
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AR020780
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                                                                                                    541 GGGGCCCTGGTAACTGTAGGGGCCCTTTTTTGCTAGCAAG 579
                                                                                                                   541 9999ccct9gtaactgtaggggccttttttgctagcaag 579
                                                                                                                                                                      481
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                                                                                                                                                                                                                                                          421
                                                                                                                                                                                                                                                                           361 caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc 420
                                                                                                                                                                                                                                                                                                                                  301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
                                                                                                                                                                                                                                                                                                                                                  301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga
                                                                                                                                                                                                                                                                                                                                                                                           241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGCCCCAGCAGCTGAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 aggctgaggcagaagggttatgtctgtggagctggccctgggggaaggcccagccggcc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGCCTCTGGTGGAAGACTTTGTAGGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
                                                                                                                                                                                                                 agtggcggctgggcggagttcacagctctatacggggacggggccctggaggaggagcacgg 480
                                                                                                                                                                           cgtctgcgggaggggaactgggcatcagtgaggaacagtgctgacggggggccgtggcactg
                                                                                                                                                          CGTCTGCGGGAAGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCCACTG
                                                                                                                                                                                                                                                                                                                                                                                                           caggittccgacgaacttttccaagggggccctaactggggccgtcttgtgggcattcttt 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
Norway, WORKING DRAFT SEQUENCE, 5 unordered pieces
                                   AC079885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539;
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Sequence 2 from patent US
AR020780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 579)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
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93.1%;
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            151212 bp DNA linear HTG
DMOSOME 4 clone RP31-246H18 strain
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Pred. No. 4.7e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208
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Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L.,
Bouffard,G.J., Karlins,E., Lee-Lin,S.-Q., Legaspi,R., Lim,M.,
Maduro,Q.L., Maduro,V.B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Prasad,A., Snyder,B., Stantripop,S.,
Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W.,
Thomas,J.W., Thomas,P.J., Walker,M.A., Wetherby,K.D. and Green,E.D.
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA on Nov 8, 2000 this sequence version replaced gi:10179358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 151212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Summary Statistics
sequencing vector: plasmid; n/a; 100% of reads
chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: phrap; version 0.990319
Consensus quality: 147800 bases at least 040
Consensus quality: 148726 bases at least 030
Consensus quality: 148733 bases at least 020
consensus quality: 149333 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 145000; agarose-fp
Insert size: 150812; sum-of-contigs
Quality coverage: 11.76x in Q20 bases; agarose-fp
Quality coverage: 11.30x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20441
20541
41010
41110
65553
                                                                                                                                                                                                                                                                                                                                                                                                                                   65653
                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/strain="Brown Norway"
                    vector_side:right"
20541. .41009
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                 clone_end:SP6
                                                                                                                                                         /clone_lib="RP31"
                                                                                                                                                                                      /chromosome="4"
/clone="RP31-246H18"
                                                                                                                                                                                                                                       /db_xref="taxon:10116"
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                      20440: contig of 20440 bp in length 20540: gap of unknown length 4109: contig of 20469 bp in length 41109: gap of unknown length 6552: contig of 24443 bp in length 65652: gap of unknown length 110365: contig of 44713 bp in length 110465: gap of unknown length 110465: gap of unknown length 151212: contig of 40747 bp in length.
                                                                                                        note="assembly_fragment"

    Genome Center

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BASE COUNT
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                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74821 GGGGCTGCCCTGTGTGCTGAGAGTGTCAACAGAAAAAATAGAGCCATTGGTGGGACAAGTG 74880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74761 TCCAACGAACTTTTCCAAGGGGCCCCAACTAGGGCCATCTTGTGACATTCTTTGTCTTT 74820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75001 AGGGAGGGAGCTCGGCATCAGTGAGGACAATACTGACTGGGGCTGTGACACTGGGGACC 75060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74941 GGCTGGGTGGAGTTCACAGCTCTATTCCGGAATGGGGCCCTAGAAGAGACATGGTGTCTG 75000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 caccaagccatgcgggctgctggagacgagtttgagacccgttttccgccgcaccttctct 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 ggctgggcggagttcacagctctatacggggacggggccctggaggaggcacggcgtctg 486
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11036
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110466. .151212
110466. .151212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACO84240 181282 bp DNA linear HTG 18-OC ACO84240 to represent the property of 
l (bases 1 to 181282)
l (bases 1 to 181282)
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Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
Beckstrom-Sternberg, S.M., Dietrich, N.L., Gupta, J., Ho, S.-L.,
Bouffard, G.G., Brinkley, C., Dietrich, N.L., Gupta, J., Ho, S.-L.,
Idol, J., Lee-Lin, S.-O., Legaspi, R., Lim, M., Maduro, Q.L.,
Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J.,
Pearson, R., Prasad; A., Snyder, B., Stantripop, S., Thomas, J.W.,
Pran, J.T., Tsurgeon, C.,
Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tran, J.T., Tsurgeon, C.,
                                                                                                                                                                                                                                                                                                                                                                  Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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BASE COUNT
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                                    Destry Match 69.7%;
Best Local Similarity 86.6%;
                    Matches 447;
                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                   50811 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0,990319 Consensus quality: 179798 bases at least Q40 Consensus quality: 180274 bases at least Q30 Consensus quality: 180274 bases at least Q20 Insert size: 138000; agarose-fp Insert size: 160000; pulse-field-gel Insert size: 150982; sum-of-contigs Quality coverage: 15.02x in Q20 bases; agarose-fp Quality coverage: 12.95x in Q20 bases; sum-of-contigs Quality coverage: 11.45x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vogt.J.L., Walker,M.A., Wetherby,K.D. and Green,E.D. NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved.
                Conservative
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5531
39504
39604
85793
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Center clone name: 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
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                                                                                                                                /note="assembly_fragment"
85893. .181282
/note="assembly_fragment"
a 36290 c 37296 g 56560
                                                                                                                                                                                                                                                                                                                        vector_side:right"
5531. .39503
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                                                                                                                                                                                                                                                                                      /note="assembly_fragment
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/db.xref="taxon:10116"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RP31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP31-103L21"
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5530: gap of unknown length
39503: contig of 33973 bp in length
39603: gap of unknown length
85792: contig of 46189 bp in length
85892: gap of unknown length
181282: contig of 95390 bp in length.
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                                                                                                                                                                                                                                 .85792
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           0; Mismatches
                         Score 405.6; DB 2
Pred. No. 8.6e-85;
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                                                DB 2;
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                                                                                                                                   325 others
                                           Length 181282;
    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 caggattggatggtggcctacctggagacacgtctggctgactggattgcacacagcagtggc 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 ggggctgccctgtgttgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtg 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 teegaegaactttteeaagggggeettaaetggggeegtettgtgggattetttgtettt 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 gacctggccgctcagctacacgtgaccccaggctcagcccagcaacgattcacccaggtt 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 caccaagccatgcgggctgctgqagacqagtttgagacccgttttccgccgcaccttctct 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99ct999c99agttcacagctctatacg999gac99g9ccct99a99ag9cacg9cgtctg 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTGGGTGGAGTTCACAGCTCTATTCCGGAATGGGGCCCTAGAAGAGACATGGTGTCTG 50224
  The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end) : R-244E17

Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC=AL132855)
                                                                                                                                                   Center: Genoscope / Centre National de Sequencage
                                                                                                                                                                                        - Web: www.genoscope.cns.fr)
On Jun 3, 2000 this sequence version replaced gi:6138746.
                                                                                                                                                                                                                            Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Hellig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Syapay,G., Saurin,W. and Weissenbach,J. Sequencing of the human chromosome 14
                                                                                             Contact: SeqRef@genoscope.cns.fr
                                                                                                                         Web site:
                                                                                                                                            Center code: GS
                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS0000B 196292 bp DNA linear PRI 22-MAY: Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence.
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----- Summary Statistics
                                                                                                                http://www.genoscope.cns.fr/
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RHdb:RH98727
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/note="matching EMBL:H79035
RHdb:RH78773
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/db_xref="taxon:9606"
/chromosome="14"
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/note="matching EMBL:AA007328
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82164. .82299
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          Identified using the e-PCR software (G. 138509. .138658
                                   dbsTs:sTS42930
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/note="matching EMBL:M78864
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RHdb:RH68657
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RHdb:RH92419
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US-09-281-131-6
PCT-US94-07089-6
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US-09-234-186-7
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1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat		SSULT 1 S-08-798-897-2 Sequence 2, Application US/08798897 Patent NO. 5789201 GENERAL INFORMATION: APPLICANT: GLASTELLA, John TITLE OF INVENTION: Genes Coding For Bcl-y TITLE OF INVENTION: Homologue NUMBER OF SEQUENCES: 5 ADDRESSE: STERNE, KESSLER, GOLDSTEIN & STREET: 1100 New York Avenue, N.W., Suitters DC COUNTRY: Washington STATE: DC COUNTRY: USA LIP: 20005 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, Version CURRENT APPLICATION NUMBER: US/08/798,897 FILING DATE: February 11, 1997 CLASSIFICATION NUMBER: US/08/798,897 FILING DATE: February 11, 1997 CLASSIFICATION NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 31,893 REFERENCE/DOCKET NUMBER: 31,893 REFERENCE/DOCKET NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 31,493.0140001 TELEFANX: 202-371-2600 TELEFAX: 202-371-2500 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 579 base pairs TYPE: nucleic acid STRANDEDNESS: both MOLECULE TYPE: cDNA 15-08-798-897-2	ALIGNMENTS	119 20.4 615 3 US-09-080-285-22 119 20.4 911 4 US-09-126-109-5 119 20.4 911 5 PCT-US93-06251-3 115.8 19.9 831 6 5459251-3 115.8 19.9 831 6 5506344-4 115.4 19.8 1274 2 US-08-461-511A-1 115.4 19.8 1274 4 US-08-461-511A-1 115.4 19.8 1274 5 PCT-US94-07089-1 115.4 19.8 1303 1 US-08-081-448-1 115.4 19.8 1303 1 US-08-081-448-7 52.6 9.0 737 1 US-08-081-48-7 52.6 9.0 737 2 US-08-616-732A-8 52.6 9.0 737 4 US-08-616-732A-8 53.6 8.7 822 1 US-08-616-732A-8 50.6 8.7 822 3 US-09-037-742B-8 50.2 8.6 624 1 US-08-248-819A-1
ctggtggcagactttgtaggttat 60 TGGTGGAAGACTTTGTAGGTTAT 60	ໝ	-y, a Bcl-2 & FOX P.L.L.C. ite 600		Sequence 22, Appli Sequence 5, Appli Sequence 3, Appli Patent No. 5459551 Patent No. 550634 Sequence 1, Appli Sequence 8, Appli Sequence 1, Appli

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           TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Guastella, John
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CITY: Wa
STATE: D
COUNTRY:
ZIP: 200
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                                            REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 14
                                                                                                         CLASSIFICATION: 424
                                                                                                                   APPLICATION NUMBER: US 08/798,897 FILING DATE: February 11, 1997
                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: herewi
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OPERATING SYSTEM: PC-DOS/MS-DOS
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202-371-2540
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                                            1483.0140002
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; STRANDEDNESS:
; TOPOLOGY: both
; MOLECULE TYPE: c
US-08-978-523-2
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  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                          NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                APPLICANT: Guastella,
                           STATE: DC
COUNTRY: US
ZIP: 20005
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LENGTH: 579 base pairs
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                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.
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wes 575; Conserv
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RESULT 4
US-08-978-523-1
US-08-978-523-1
; Sequence 1, Application US/08978523
; Patent No. 5883229
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SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
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TELEPHONE: 202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 14
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STRANDEDNESS: both
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                                                                                                                                                                                                          361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420
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541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTTGCTAGCAAG 579
              541 ggggccctggtaactgtaggggccttttttgctagcaag 579
                                                                   481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG
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; MOLECULE TYPE: US-08-978-523-1
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APPLICANT: Guastella, John
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
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                                                                                                                                                                                                                                121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180
                                                                                                                                                                                                                                              121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
301
                                                                         301 gtctttggggctgcactgtgttgctgagagtgtcaacaaggagatggaaccactggtggga 360
                                                                                                                                 241 caggtctccgacgaactttttcaagggggccccaactggggccgccttgtagccttcttt 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/798,897
                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                               1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                                       GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM FOR COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
218 gctcagcccagcaacgcttcacccaggtctccgacgaactttttcaagggggccccaact 277
                               424 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGGCTCCACATCACCCCAG 483
                                                          158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
                                                                                              FEATURE:
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APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis General Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
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                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                   NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: No. 5646008thrup, Thomas E. REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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ZIP: 60610
                                                                                                                                                                                                                                                                    LOCATION:
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TELEFAX: 312-755-4489
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                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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                                                                                                                                                               0; Mismatches 190; Indels
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                                                                                                                                                                              Score 131; DB 1; Length 926; Pred. No. 2.2e-25;
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; LOCATION: US-08-470-670A-6
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Patent No. 5834309 5710045
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APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08470670A
                                                                                                                                                                     TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO:
                                  FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US OF
APPLICATION NUMBER: US OF
PTITING DATE: 22-JUN-1993
                                                                                                                                                                                                                             NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: AR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: 77210
                                                                       TOPOLOGY:
                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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                  135..836
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98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157

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Score 131; DB 2; Length 926; Pred. No. 2.2e-25;

Match 22.5%; Local Similarity 56.3%;

245;

Conservative

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              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHANE: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS FOR ENHANCING I CELL SURVEY TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          724 ACAATGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783
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                                                                                                                                                  FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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SEQUENCE CHARACTERISTICS:
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STATE:
                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Relccc
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                                                                                               REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: RPI-034CP
                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                NAME: DeConti, Giulio A. (GAD)
REGISTRATION NUMBER: 31,503
                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      June, Carl H. and Thompson, Craig B. VENTION: METHODS FOR ENHANCING T CELL
                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAHIVE & COCKFIELD
                                                                                                                                                                           NUMBER: US 08/435,518
04-MAY-1995
                                                                                                                                                                                                                                     07-JUNE-1995
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09167921A patent No. 6172216
                                                                                                                                                                                                                                                                                                                                                                   ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 22.5%;
Best Local Similarity 56.3%;
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                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/167,921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                         APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
                                                                                                                                                                                                                                                                                                              APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
                                                                                                                                                                                                                                       FILE REFERENCE: ISPH-0324
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION IMFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                          ORGANISM: Homo sapiens
                                                                        FEATURE:
                                                                                                           TYPE: DNA
                                                                                                                             LENGTH: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggctacctggagacgc 397
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Pred. No. 2.2e-25;
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US-09-167-921-1

DATABASE ENTRY DATE: 1994-07-26

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CURRENT APPLICATION NUMBER: US/09/277,020
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
US-09-277-020-39
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                                                                                                                                      Matches 245;
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39, Application US/09277020 Patent No. 6210892
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation TITLE OF INVENTION: of mRNA Processing FILE REFERENCE: ISPH-0339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bennett, C. Frank
158 togagacocgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
                                                  98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
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                                                                                                                                          22.5%; Score 131; DB 4; Length 926; 56.3%; Pred. No. 2.2e-25;
                                                                                                                         0; Mismatches 190; Indels
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CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT ETLING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (135)...(836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-323-743-1
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Best Local Similarity 56.3%;
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APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett p.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 926
218 gctcagcccagcaacgcttcacccaggtctccgacgaactttttcaagggggccccaact 277
                                          424 ttgaactgcggtaccggcgggcattcagtgacctgacatcccagctccacatcaccccag 483
                                                                   158 tegagaecegetteeggegeaeettetetggeggeteagetggatgtgaececag 217
                                                                                                                                98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
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                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                     Score 131; DB 4; Length 926; Pred. No. 2.2e-25;
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                                                                               NAME/KEY: CDS
LOCATION: 135..836
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-461-511A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08461511A Patent No. 6303331 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/461,511A
APPLICATION NUMBER: US/08/461,511A
FILING DATE: 05-Jun-1995
FILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:179
REFERENCE/DOCKET NUMBER: ARCD:179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 414-7577
INFORMATION FOR SEQ ID NO: 6:
INFORMATION FOR SEQ ID NO: 6:
Best Local Similarity 56. Matches 245; Conservative
                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                         LENGTH: 926 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boise, Lawrence H.
                       22.5%; Score 131; DB 4; 56.3%; Pred. No. 2.2e-25;
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         Mismatches 190;
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                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATION OPERATION SYSTEM: PC-DOS CURRENT APPLICATION UMBER: PCT, APPLICATION UMBER: PCT, FILING DATE: CONCURRENTI
                                                                                           TELEPHONE: 512-320-720
TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/01 FILING DATE: 22 JUNE 199: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP:
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                                                                                                                                                                                           NAME: PARKER, David L. REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION
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                                          TYPE: nucleic acid
STRANDEDNESS: sing
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                               TOPOLOGY: linear
                                                                               ENGTH:
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                                                                                     926 base pairs
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SYSTEM: PC-DOS/MS-DOS, ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                         UMBER: PCT/US94/07089
CONCURRENTLY FILED
                                                                                                                                                                                                                                                                       22 JUNE 1993
                                                  single
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Compositions and Methods
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US-08-465-485A-20
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                                                COMPUTER: IBM PC COMPUTER:
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-70N-1995
S14
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Regulation of bcl-2 Gene Expression NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                  APPLICATION NUMBER: US OF FILING DATE: 20-SEP-1993
                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                      STREET: 1755 S. CITY: Arlington STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                                                                                                                                                                              Virginia
                                                                                                                                                                                                                                                                                       1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                            Reed, John
                                                                                                                                                                                                                                                                                                                          OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
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135..836
                               US 08/124,256
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US-09-080-285-20
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                                                                                                                                                                                         Sequence 20, Application US/09080285 Patent No. 6040181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
US-08-465-485A-20
                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                             APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO:
         STREET: 1755 S. Jefferson Davis Hwy., Suite 400 CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                               604 TACGG 608
                                                                                                                                                                                                                                                                                                                                 451 tacgg 455
                                                                                                                                                                                                                                                                                                                                                     544 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 603
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                  ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                         484 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 543
                                                                                                                                                                                                                                                                                                                                                                                                                                              331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 accccaggctcagcccagcaacgcttcacccaggtctccgacgaactttttcaagggggc 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 gatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtg 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 GOGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 303
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FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 gctggccccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctgga 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME:
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Best Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/0
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (408) 436-2075 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 20-SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
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LENGTH: 717 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                      304
                                                                                                                                                                                                                                                                                                                                                                                                    244 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 303
                                                                                                                                                                                                 APPLICATION NUMBER: US 01 FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
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                                                                                                                                                     331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg
                                                                                                                                                                                                                      271 cccaactggggccgccttgtagccttctttgtctttggggctgcactgtgtgctgagagt 330
                                                                                                                                                                                                                                                                                                    211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
604 TACGG 608
                              451 tacgg 455
                                                                 544 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG
                                                                                                                                 484 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 58.6 nes 214; Conservative
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                                                                                                                                                                                                                                                                 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGACGAGCTCTTCAGGGACGGG 423
                                                                                      gagacgcggctggctgactggatccacagcagtgggggctgggcggagttcacagctcta 450
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tsujimoto, Yoshide; Croce, Carlo A. TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                    1942 gtcaaccgggagatgtcgcccctggtggacaacatcgccctgtggatgactgagtacctg
                                                                                                                                                                                                         1822 acgcccttcaccgcgcggggacgctttgccacggtggtggaggagctcttcagggacggg 1881
                                                                                                                                                                                                                                                                                                                                                   1702 gcggggcctgcgctcagcccggtgccacctgtggtccacctggccctccgccaagccggc 1761
                                                               2002 aaccggcacctgcacacctggatccaggataacggaggctgggatgcctttgtggaactg 2063
2062 tacgg 2066
                                                                                                                                                                                                                                                                                                                                                                        151 gatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtg 210
                                                                                                                                                         331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg 390
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 994,941
FILING DATE: 23-DEC-1992
APPLICATION NUMBER: 663,010
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: 883,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 18-APR-1994
                                                                                     391 gagacgcggctggctggattggattccacagcagttgggggctgggcggagttccacagctcta 450
                                                                                                                                                                                                                                 271 cccaactggggccgccttgtagccttctttgtctttggggctgcactgtgtgctgagagt 330
                                 451 tacgg 455
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Local Similarity 58.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4825
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pred. No. 3.4e-23;
0; Mismatches 151;
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 3 3 4 4 4 7 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
554.8 553.2 527.6 527.6 527.6 428.2 4400.2 380.2 380.2 380.2 386.2 386.2 386.2 294.2 294.2 294.2 294.2 294.2	Score
95.2 90.5 90.5 90.5 90.5 63.3 63.3 50.6 50.5 50.3 50.5 50.5 50.5 50.5 50.5 50.5	% Query Match Length DB
804 1030 1449 3487 697 643 815 792 540 758 601 749 362 433 457	ength D
10 10 10 10 10 10 10 10 10 10 10 10 10 1	1
AL157542 BE793530 AK001564 AK001564 AK004680 B1970566 B1910270 BF785386 AK013244 B2298789 AW258810 B1764428 B1764428 B2764905 AG677345 AA596919 AW326901 BB856021 BB856021 BB816021	ID
AL157542 DKF2P761D BE793530 601590016 AK015644 Mus muscu AK015644 Mus muscu BI770566 603060362 BI910270 603069493 BF785386 602111728 AK013244 Mus muscu BG298789 602396527 AW258810 um74a02.y BI764428 603050701 BF204905 601866718 BG2677345 602624059 AA596919 vo211608.r AW326901 20104 MAR BH856021 BB856021 BM191403 daj86a10.	Description

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20.9	20.9 20.9	21.1	21.6	21.9	22.2	22.	23.3		26.9 5.1	
973 808	1035 836	642 642	513 404	699 974	700 697	5 T S	862	624	447 628	473 612 431
10 10	10	995	10	10	10	3 5	10	99	12	0
	BI409987 BM018295	w »	BM363392 AI716839 BG824757	BE250036	BG831301 BI457116	BG244400	BG973530	BE188975 AL632408	BB851239 AQ532175 AQ665088	BE647090 BE508939 AW048567 AW159063
BG18Ub/1 0U2329440 BI222971 602943462		AL537680 AL537680 BB163814 BB163814 BJ060637 BJ060637	AI716839 UI-R-Y0-a BG824757 602728745	BE870269 601447403 BE250036 600943041			BG973530 602842233 BG244406 602356535	BE188975 db62a05.x AL632408 AL632408 AO401160 HS 5062_A		BE647090 UI-M-BH1- BE508939 dc14h09.y AW048567 UI-M-BH1- AW159063 za50h02.x

ALIGNMENTS

BASE COUNT	FEATURES SOURCE	REFERENCE AUTHORS TITLE JOURNAL COMMENT	
/organism="Homo sapiens" /db_xref="taxon:9606" /clone=NKFZp761D0816" /clone_lib="761 (synonym: hamy2)" /tissue_type="amygdala" /dev_stage="adult" /lab_host="DH10B" /note="Vector: pSport1; Site_1: Not1; Site_2: Sall" /10 a 217 c 294 g 142 t 1 others	lopfer is th e from arch C enced enced elberg an Ger 1 sequ clone ise cor	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mases 1 to 804) Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S. EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.) Unpublished (1999) Contact: Ansorge W MIPS	AL157542 BO4 bp mRNA linear EST 24-FEB-2000 DKFZp761D0816_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D0816 5', mRNA sequence. AL157542 AL157542.1 GI:7057943 EST. Homo sapiens

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   cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; (bases 1 to 1030)
NIH-MGC http://mgc.nci.nih.gov/.
Plate: LLCM800 row: p column: 04
                                                                                                                             Contact: Robert Strausberg, Ph.D.
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Pred. No. 6.3e-116;
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DEFINITION AK015644 RESULT

AK015644 1949 bp mRNA linear HTC 19-3 Mus musculus adult male testis cDNA, RIKEN full-length enrical library, clone:4930488D08:Bcl2-like 2, full insert sequence

RNA linear HTC 19-JAN-2002 RIKEN full-length enriched

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                   541 9999ccct99taactgtag9g9gcctttttttgctagcaagtga 582
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284 c 386 g 170 t
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/cell_line="MGC3"
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/clone_lib="NIH_MGC_7"
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Pred. No. 1.6e-115;
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                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Rax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RIKEN Genome Exploration Research Group Phase II Team and the
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Hayashizaki,Y.
                                                                                                                                                                                                                                                           please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                   further details
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/db_xref="G1:12854053"
/translation="MATPASTDURALVADEVGYKLROKGYVCGAGPGEGPAADPLHO
/translation="MATPASTDURALVADEVGYKLROKGYVCGAGPGEGPAADPLHO
AMRAGDEFETRERETESDLAAQLHVTPGSAQQRETOVSDELFQGGPNMGRLVAFFVF
GAALCAESYNKEMEPLVGQVQDMWVAYLETRLADWIHSSGGMAEFTALYGDGALEEAR
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Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer second cenome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409, 685-690 (2001) 5 (bases 1 to 3487)
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High-efficiency full-length cDNA cloning
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Mus musculus adult male lung cD
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241 caggtctccgacgaactttttcaagggggccccaactggggccgccttgtagccttcttt
                                                                  181 ttctctgatctggcggctcagctgcatgtgaccccaggcttagcccagccaacgcttcacc 240
                                                                                                                                  329 CCGCTGCACCANGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
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                                                                                                                                                                                                                                                                                                                  209 ATGGCGACCCCAGCCTCAACCCCAGACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 268
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                                                 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACC
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Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      further details.
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/db_xref="GI:12836028"
/translation="MATPASTPDTRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQ
AMRAAGDEFETRERRTFSDLAAQLHVTPGSAQORFTQVSDELFQGGPNWGRLVAFFVF
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/note="Bcl2-like 2
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5',
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                                                         /note-"Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size type cloning). Average insert size and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is with wor there?
                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5209862"
/clone_lib="NIH_MGC_122"
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                           this is a NÍH_MGC Library."
202 c 248 g 126 t
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                    Email: cgapbs r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11548 row: j column: 23
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                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                         Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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       High quality sequence stop: 643.
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Pred. No. 7.9e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                            440 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGCATGGAACCACTGGTGGG 499
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                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Unpublished (1999)
      National Institutes of Health, Mammalian Gene Collection (MGC)
                                    NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                Mus musculus
                                                                                                                                                                                                                     602111728F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
                                                                                                                                                                       BF785386.1 GI:12090422
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                                                                                                                                    house mouse
                                                      mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; (bases 1 to 815)
                                                                                                                                                                                                           mRNA sequence.
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/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:5218294"
/clone_lib="NH_MGC_118"
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94.3%;
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                                     561 ggccttttt 569
                                                                                474
                                                                                         501 ggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctgggtaactgtagg
                                                                                                                                             416 CACAGCTCTATACGGGGACGGGCCCCTGGAGGAGGCACGG-GTCTGCGGGAGGGGAAC-G
                                                                                                                                                                 441 cacagetetatacggggacgggggcettggaggaggcgcgggggtetgcggggagggaactg 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 tgtctgtggagctggccccggggagggcccagcagctgacccgctgcaccaagccatgcg 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 cccagacacacgggctctggtggcagactttgtaggttataagctgaggcagaagggtta 80
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                                                                  GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACT-GGGGCCCTGGTAACTGTAGG
GGCCTTTTT 541
                                                                                                                                                                                                                                                                                                      TGCTGAGAGTGTCAACAAAGAAATGGAGCC-TTGGTGGGACAAGTGCAGGATTGGATGGT
                                                                                                                                                                                                                                                                                                                             tyctgagagtgtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggt 380
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                                                                                                                                                                                                                                                                                                                                                                                 CCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGGCATTCT---TGTCTTGGGGCTGCCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggcagctggagatgagttcgagacccgcttccggcgcaccttctctctgatctggcggctca 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: LLAM9853 row: h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone="IMAGE:4239798"
/Clone_lib="NCI_CGAP_Kid14"
/Lab_host="NHIOB (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally primer: Oligo dT
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
a 212 c 296 g 141 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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Nature 409, 685-990 (2001)
5 (bases 1 to 854)
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                                                                                            Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Tax:81-45-503-9216)
                                                              Please visit our web site (http://genome.gsc.riken.go.jp/) for
cDNA library was prepared and sequenced in Mouse Genome
                                        further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN Genome Exploration Research Group Phase II Team and the
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Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer prepare mouse tissues. First strand cDNA was primed with a primer prepared by using trehalose thermo-activated reverse transcriptase prepared by using trehalose thermo-activated reverse transcriptase prepared by using trehalose thermo-activated reverse transcriptase through one round of normalization to Rot = 7.5 and subtraction to through one round of normalization to Rot = 7.5 and subtraction to
                                                                                                                                                                                                                                                                                           ttetetgatetggeggeteagetgeatgtgaceceaggeteageceageaaegetteaee 240
                                                                                                                                                                                                                                                                                                                                                         CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 315
CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 615
                          Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5'
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196. .732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Protein_id="BAB28740.1"
/Protein_id="BAB28740.1"
/db_xref="GI:12850488"
/translation="MATPASTPDTRALVADFYGYKLROKGYVCGAGPGEGPAADPLHQ
/translation="MATPASTPDTRALVADFYGYKLROKGYVCGAGPGEGPAWGRLVAFFVF
AMRAAGDEFETRERETESDLAAQLHVTPGSAQQRETQVSDELFQGGPWWGRLVAFFVF
GAALCAESVNKEMEPLYGQVQDWMVAYLETRLADWIHSSGGWVRSSQLLLLSASLYKVG
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/note="Bcl2-like 2
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92.4%;
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301 gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
                                          338 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCCATTCTTT 397
                                                                241 caggtctccgacgactttttcaagggggccccaactggggccgccttgtagccttcttt 300
                                                                                                                         279 TTCTCTGACCTGGC-GCTCAGCTACACGTGACCCCAGGCTCAGCCAGCAACGCTTCACC 337
                                                                                                                                               181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagccaacgcttcacc 240
                                                                                                                                                                                                                              121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                                                                                                                                                                                                     159 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10394 row: e column: 08
High quality sequence stop: 713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 792)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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//Aab_host="DH10B (phage-resistant)"
//Aab_host="DH10B (phage-resistant)"
//Inote="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Note: this is a NIH_MGC Library."
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/clone_lib="NIH_MGC_94"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/WashU-NCI Mouse EST Project 1999
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1 (bases 1 to 540)
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IMAGE:2300906 5' similar to SW:BCLW_MOUSE P70345 APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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/dev_stage="adult"
//dev_stage="adult"
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/sex="female"
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/clone="IMAGE:2300906"
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Best Local Similarity

62.1%; 91.6%;

Score 362; DB 9; Pred. No. 3.2e-72;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 gtctttggggctgcactgtgtgctgagagtgtccaacaaggagatggaaccactggtggga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 agtgggggct 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 aagetgaggcagaagggttatgtctgtggagctggccccgggggagggcccagcagctgac 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caggtotocgacgaactttttoaagggggcoccaactggggcoccottgtagcottottt 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGGCCGTCTTGTGGCATTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /58 bp mRNA linear EST 25-SEP-2001 603050701F1 NTH_MGC_116 Homo sapiens cDNA clone IMAGE:5190792 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI764428.1 GI:15756006
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                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11477 row: a column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 758)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                 quality sequence stop:
         /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); source anonymous pool of 3 colons, age 26 yo male, 49
                                                                                                    /clone="IMAGE:5190792"
                                                                                 /clone_lib="NIH_MGC_116"
                                                                     /lab_host="DH10B"
                                                                                                                        /db_xref="taxon:9606"
                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                               ocation/Qualifiers
71 yo male colon; 46 yo male kidney, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 gtctttggggctgcactgtgtgctgagagtgtcaacaa 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 caggtotocgacgaactttttocaagggggccccaactggggccqccttgtagccttottt 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601866718F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106836 5',
                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                       Plate: LLCM987 row: d column: 05 High quality sequence stop: 561.
                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM987 row: d column: 05
                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                      cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc. clone distribution information can clone distribution information can
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/clone="IMAGE:4106836"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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98.2%;
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Pred. No. 1.5e-64;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGTCTCCGATGAACTGTTTGCAAGGGGGCCCCCAACTGGGGTTCGCTTGTAGCCTTCTTG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388;
                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           602624059F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4748943 5',
                                                                                                                                                                                                                                                                                                                                                            BG677345.1 GI:13908742
                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG677345
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/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhOI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 176 c 201 g 114 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                           749 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 01-MAY-2001
                                                                                                                                                                                                                                              Homo
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                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 caggtctccgacgaactttttcaagggggccccaactggggccgccttgtagccttctt 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 TICTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTCCACC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ttetetgatetggeggeteagetggeatgtgaeceeaggeteageecageaaegetteaee 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccggcttccggcgcacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 aagctgaggcagaagggttatgtctgtggagctggcccgggggagggcccagcagctgac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 50.5%;
Local Similarity 99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 245
                                                   Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHM Mouse EST Project
WashU-HHM Mouse EST Project
Washington University School of Medicinep
4444 Poiest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                 Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA596919 362 bp mRNA linear EST 19-SEP-19: vo21f08.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1050567 5' similar to TR:E123735 E123735 Rl MRNA. ;, mRNA
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                          314 286 1800
314 286 1810
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mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="squamous cell carcinoma"
/tlab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pcWV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 239 c 219 g 135 t
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/db_xref="taxon:9606"
/clone="IMAGE:4748943"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_Skn4"
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Pred. No. 8.7e-57;
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BASE COUNT
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                                                                                                  ORGANISM
                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147
                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 ctgcaccaagccatgcgggcagcttggagattggagttcgagacccgcttccggcgcaccttc 183
                                                                                                                                                                                                                                                                                         327
                                                                                                                                                                                                                                                                                                        304 tttggggctgcactgtgtgctgagagtgtcaacaag 339
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                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGAACTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAG
                                                                                                                                                                                                                                                                                                                                                        GTTTCCGACGAACTTTTCCAAGGGGCCCTAACTGGGGCCCGTCTTGTGGCATTCTTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                       totgatotggoggotoagotgoatgtgaccccaggotoagoccagcaacgottcacccag 243
                                                                                                                                                                                                                                                                                         TTTGGGGCTGCCCTGTGTGCTGAGAGTGTCACAAAG 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                  Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                   AW326901.1 GI:6762822
EST.
                                                                                                                                                                   AW326901
                                                                                                                                                                                     20104 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                       AW326901
   Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
                                                                                                                    COW
Casas, E., Wray, J.E., White, J.,
                                                    Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer: -28ml3 rev2 ET from Amersham
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                                  (bases 1 to 433)
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/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
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91.4%;
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                                                                                                                                                                                                                                                                                                   154 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTAGTGGCAGACTTTGTGGGCTAT 213
274
                                                                         334 TICTCCGATCTGGCAGCTCAGCTGCATGTGACCCCGGGCTCGGCCCAGCAACGCTTCACC
                                                                                                                 181
                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                       1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                                                                                            AAGCTGAGGCAGAAGGGGTATGTTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC
                                                                                                                                                CCGCTACACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 333
                                                                                                                                                                      ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                           ttototgatotggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
                                                                                                                                                                                                                                                                                                                                                                                 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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21180013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 10 row: G column: 24
Seq primer: ATTTAGGTGACACTATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV SPORT5; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
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/lab_host="DH10B"
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AF216205 Sus scrof
AJ001203 Sus scrof
AF245488 Bos tauru
AF245489 Bos tauru
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AX030819 Sequence
AL049829 Human chr
AC079885 Rattus no
AC084240 Rattus no
AX345130 Sequence
X82462 X.laevis R1
AX345131 Sequence
U10579 Rattus norv
BD006625 A mutagen
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AB073983 Canis fam
AX005131 Oryctolag
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION TITLE
JOURNAL
MEDLINE
REFERENCE REFERENCE ACCESSION KEYWORDS ORGANISM AUTHORS JOURNAL AUTHORS Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)
Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
bcl-w, a novel member of the bcl-2 family, promotes cell survival
Oncogene 13 (4), 665-675 (1996)
96358615 Human Bcl-w (bcl-w) mRNA, complete cds. U59747 Direct Submission Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne 2 (bases 1 to 582) Gibson, L., Holmgreen, S.P., U59747.1 GI:1572492 HSU59747 Cory,S. 582 bp Huang, D.C.S., Bernard, O., Adams, J.M. mRNA linear PRI 29-SEP-1996

SOURCE

VERSION

Result

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Match Length DB

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TITLE

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/Protein_10" ABD9055.1"
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GAALCAESVNKEMEPLYGQVOEWMYAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagccaacgcttcacc 240
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                                                                         TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC
                                                                                                                                           CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGGCTTCCGGCGCACC 356
                                                                                                                                                                                                                AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
                                                                                                                                                                                                                                                                                                                                                             581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Rese
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohara, O., Nagase, T., Kikuno, R. and Nomura, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 3542)
Nagase,T., Sekl.N., Ishikawa,K., Ohira,M., Kawarabyasi,Y., Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N. Prediction of the coding sequences of unidentified human genes. V The coding sequences of 80 new genes (KIAAO201-KIAAO280) deduced analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens male brain myloblast cell_line:KG-1 cDNA to mRNA, clone_lib:pSPORT 1 clone:HA6752.
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D87461.1 GI:1944417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEEETRERRTESDLAAQLHVTPGSAQQRETQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLYGQVOEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR RLREGNWASVRTVLTGAVALGALVTVGAFFASK"

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177. .7
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177. .758
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/db_xref="GI:1944418"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (A24428)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to human transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="KIAA0271"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="brain"
/clone_lib="pSPORT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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99.7%;
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Pred. No. 1.1e-118;
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protein bcl-2

Gaps

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aagctgaggcagaagggttatgtctgtggagctggcccgggggagggcccagcagctgac 120
                                                            CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
                                                                                                                                                                                  ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
                                                                              cogotycaccaagccatycygygcagctygagatyagttcygagacccyottccygcgcacc 180
                                                                                                                       AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6 from Patent EP0932674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes Patent: EP 0932674-A 6 04-AUG-1999; AMRAD OPERATIONS PTY LTD (AU)
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                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAC07880.1"
/protein_id="CAC07880.1"
/db_xref="G1:10046126"
/translation="Matpasapdtralvadfvgyklrokgyvcgagegegeaadplho
Amraagdefetrefrretsdlaaolhytpgsaooretroysdelfoggenwgrlvafflf
GAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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                              AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
                                               aagctgaggcagaagggttatgtctgtggagctggcccgggggagggcccagcagctgac 120
                                                                                            Sequence 6 from AX030817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes Patent: WO 9735971-A 6 02-OCT-1997;
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RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unidentified"
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99.5%;
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Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich, N.L., Guan,X., Gupta,J., Ho,S.-I., Karlins,E., Legaspi,R.,
Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Clone distribution: MGC clone distribution information can be fo
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 15 Row: k Column: 19
                                                                                                                                                                                                                                                                                  DNA Sequencing by: Nations Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                            Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                           Web site:
                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                http://www.nisc.nih.gov/
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                                           information can be found
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IMAGE:3944307, mRNA,
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AMRAAGDEFETRFRRTFSDLAAGLHVTFGSAQDKFTQVSDELFQGGPNMGRLVAAFFVF
GAALCAESVNKEMEPLYGQVQEMWAYLETRLADWIHSSGGMAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALYTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Lung, small
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/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="LocusID:599"
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AR020780
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Patent: US 5789201-A 2 04-AUG-1998;
Location/Qualifiers
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                                                                                           gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
                                                                        CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC
AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCCTGGAGGAGGCACGG
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/protein_id="AAC64200.1"
/db_xref="G1:3747130"
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GAALCAESUNKEMEDIVGQVQDWNVTYLETRLADWIHSSGGWAEFTALYGDGALEEAR
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/db_xref="taxon:10116"
/tissue_type="brain"
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Pred. No. 4.3e-107;
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                                                                                     ttototgatotggcggctcagctgcatgtgaccccaggctcagcccagcaacgattcacc
                                                                                                                                         CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                                                                                           ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                                                                                                                                                aagctgaggcagaagggttatgtctgtggagctggcccgggggagggcccagcagctgac 120
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                                                                       AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC
                                                                                                                                                                                                                                                                                  ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT
                                                                                                                                                                                                                                                                                                                                                               548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (03-JUN-1996) Molecular Biology Unit, The Walter at Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    582 bp
Mus musculus Bcl-w (bcl-w) mRNA,
U59746
U59746.1 GI:1572494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 582)
Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,
Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.
bcl-w, a novel member of the bcl-2 family, promotes cell survival
Oncogene 13 (4), 665-675 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Protein_id="AAB09056.1"
/Protein_id="AAB09056.1"
/Gb_xref="GI:1572495"
//translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
//translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
//translation="MATPASTPDTRALVADFVGYCGAGPGEGPAADPLHQ
AMRAGOBETPRERTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVQDMYVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
a 158 c 200 g 117 t
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/db_xref="taxon:10090"
/chromosome="14"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 3476)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-OCT-1997) Center for Molecular Medicine, Emory University, 1462 Clifton Road, Atlanta, GA 30322, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bcl-w is required for testis homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Ross, A.J. and MacGregor, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse
             /protein_id="AABB6430.1"
//brotein_id="AABB6430.1"
//db_xref="G1:262320"
//tans1ation="MarpaSTPDTRALYADFVGYKLROKGYVCGAGPGEGPAADPLHQ
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AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVQDWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVTVLTGAVALGALVTVGAFFASK"
611. .3476
                                                                                                                                                                                                                  /number=2
171. .610
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/10J"
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                                                                                                                                                                                                                                                                                                                                                                        /chromosome="14"
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/gene="Bcl-w"
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                                                                                                                                                                   Sequence 8 from Patent EP0932674.
                       l (bases 1 to 581)
Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. Anovel mammalian gene, bcl-w, belongs to the bcl-2 apoptosis-controlling genes Patent: Ep 032674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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/gene="BC1-W"
/note="mRNA destabilization element"
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1 (bases 1 to 581)
Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
A novel mammalian gene, bcl.w, belongs to the bcl-2 family of
                                                                      unclassified
                                                                                     unidentified
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GAALCAESVNKEMEPLVGQVODWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR
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                                                                                       Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11 from chromosome 14 of use of the control of the
AL049829.4 GI:8217859
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                                        from chromosome 14 of Homo sapiens (Human), complete sequence
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Patent: WO 9735971-A 8 02-OCT-1997;
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU) ; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
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/db_xref="taxon:32644"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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On Jun 3, 2000 this sequence version replaced gi:6138746.
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Direct Submission
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                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
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RHdb:RH102162
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/note="matching EMBL:AA007328
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RHdb:RH98727
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                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717 grovemont Circle, Galthersburg, MD 20877, USA On Nov 8, 2000 this sequence version replaced gi:10179358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
Boulfard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Gupta, J.,
HO, S.-L., Idol, J., Karlins, E., Lee-Lin, S.-Q., Legaspi, R., Lim, M.,
Maduro, C.L., Maduro, V.B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Prasad, A., Snyder, B., Stantripop, S.,
Thomas, J.W., Thomas, P.J., Tiongson, E.E., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D.
NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T51212 bp DNA linear HTG 08-NO Rattus norvegicus chromosome 4 clone RP31-246H18 strain Brown Norway, WORKING DRAFT SEQUENCE, 5 unordered pieces.

AC079885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 151212)
Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 147800 bases at least Q40 Consensus quality: 148726 bases at least Q30 Consensus quality: 14933 bases at least Q20 Insert size: 145000; agarose-fp Insert size: 150812; sum-of-contigs Quality coverage: 11.76x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 151212)
                                                                                                                                                                                                                                     Center clone name: 246H18
                                                                                                                                                                                                                                                                                                     Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                               Center project name:
                                                                                                                                                                                                                                                                                                                        Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                             Center: NIH Intramural Sequencing Center Center code: NISC
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74875 CAAGTGCAGGATTGGATGGTGGCCTACCCAGAGACACGCCTGGCTGACTGGATCCACAAC 74934
                                                                                    74815 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAGAAAAATAGAGCCATTGGTGGGA 74874
                                                                                                                                                                  74755 CAGGTTTCCAACGAACTTTTCCAAGGGGCCCCAACTAGGGCCATCTTGTGACATTCTTT 7481
                                                                                                                                                                                                                                                     74695 TTCTCTGACCTGGCCACTCAGCTACATGTGATGCCAGGCTCAGCCCAACAATGCTTCACC 7475
                                                                                                                                                                                                                                                                                                                                       74635 CTGATACACCAAGCCATGTGGGCTGCTGGAGACAAGTTAGAGACCCCACTTCCAGCACACC 74694
                                                                                                                                                                                                                                                                                                                                                                                                                       74575 AATCCCAGACACATGGGCTCTAATGGTTGAGCTGGCCCCGGGGAAGGCCCAACAGCCAAC 74634
                      301 gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
                                                                                                                                                                                               241 caggtctccgacgactttttcaagggggccccaactggggccgccttgtagccttcttt 300
                                                                                                                                                                                                                                                                             181 ttetetgatetggeggeteagetgeatgtgaccecaggeteageceageaacgetteaec 240
                                                                                                                                                                                                                                                                                                                                                             121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will
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110466. 151212
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a 30838 c 31177 g 45417 t
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/chromosome="4"
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/strain="Brown Norway"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%; Score 388.6; DB 2
83.9%; Pred. No. 1.9e-76;
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AC084240
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Norway, WORKING DRAFT SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                   * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is so not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                       Sequencing vector: plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Assembly program: Phrap; version 0.990319
Consensus quality: 179798 bases at least 040
Consensus quality: 180132 bases at least 030
Consensus quality: 180132 bases at least 020
Insert size: 18000; agarose-fp
Insert size: 18000; pulse-field-gel
Insert size: 160000; pulse-field-gel
Insert size: 180982; sum-of-contigs
Quality coverage: 12.95x in 020 bases; pulse-field-ge
Quality coverage: 11.45x in 020 bases; sum-of-contig:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 181282)
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Center clone name: 103L21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----- Summary Statistics
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5430: contig of 5430 bp in length 5530: gap of unknown length
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4 clone RP31-103L21 strain Brown
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FEATURES
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Best Local Similarity 83.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49799 ANTCCCAGACACATGGGCTCTAATGGTTGAGCTGGCCCCGGGGGAAGGCCCCAACAGCCAAC 49858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49859 CTGATACACCAAGCCATGTGGGCTGCCTGGAGACAAGTTAGAGACCCACTTCCAGCACACC
                                                                                                                                                                                                                                                                              50039 GTCTTTGGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAGAAAAATAGAGCCATTGGTGGGA 50098
                                                                                                                                                                                                                                                                                                                                                   49979 CAGGTTTCCAACGAACTTTTCCAAGGGGGCCCCAACTAGGGCCCATCTTGTGACATTCTTT 50038
                                                                                                                                                                                                                                                                                                                                                                                                                        49919 TTCTCTGACCTGGCCACTCAGCTACATGTGATGCCAGGCTCAGCCCAACAATGCTTCACC 49978
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                                                                                                                                       50159 ANTGGGGGCTGGGTGGAGTTCACAGCTCTATTCCGGAATGGGGCCCTAGAAGAGACATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                                                                           421 agtgggggctgggcggagttcacagctctatacgggggacgggggcctggaggaggcggg 480
                                                                                                                                                                                                          301 gtctttggggctgcactgtgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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39604._.85792
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/chromosome="4"
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39603: gap of unknown length
85792: contig of 46189 bp in length
85892: gap of unknown length
181282: contig of 95390 bp in length
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Pred. No. 1.9e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 others
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0;

49918

Search completed: June 6, Job time: 7495 sec

2002, 11:58:14

50218

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OM nucleic - nucleic search, using sw model
N. Geneseq_032802:*

N. Geneseq_032802:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 08
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|: \sinsi\gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
|: \sinsi\gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

98765AUNP	Result No.
578.2 578.2 577.8 572.6 572.6 527.8 527.8 527.8	Score
99.2 99.2 98.2 98.2 90.5 90.5	Query Match Length DB
583 589 579 579 579 579 581	ength DB
18 20 20 19 20 20 20 20	
AAT96577 AAX25134 AAX25132 AAV28334 AAX15946 AAV28333 AAX15945 AAX25133 AAX15945	ID
Human bcl-w DNA. Human bcl-w gene d Human bcl-w gene. Human bcl-y gene. cDNA encoding the Rat bcl-y gene. R cDNA encoding the Mouse bcl-w gene. Mouse bcl-w gene.	Description

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5086 5087 5105 7996	5086 5086	720 765	747 720	720	1236	926	926	926	926	636 702	1742	150	150	150	150	150	150	150	6049	6049	1864	1098	581
19 22 9 20	15	22 14	22	222	22	22	21	17	16	2 2 2	22	22	22	22	2 6	2 2 2	22	22	24	24	19	19	20
AAX75766 AAD15284 AAN81292 AAX33184	AAQ54631 AAQ86661	AAH45294 AAQ49815	AAF30926 AAH45293	AAH45295	AAS00247	AAC90810	AAZ93614	AAT40079	AAQ81698	AAH48169 AAH43464	AAF75960	AAI05940	AAI45438	AAI20236	AAN 13003	ABA32370	ABA65269	ABA47382	ABL32229	ABL32228	AAV59630	AAV41925	AAX25135
	bcl	DNA encoding numan Bcl-2. Homo sapie Bcl-2 DNA fragment	n Bcl-xL n Bcl-2 c	m o	Bc1-X1-DTR apoptos	Human Bcl-xL nucle	BC1-x gene. "O"O Human bc1-x cDNA.	XL gene.	n thymus B	lone HP0356	Mutant hol-XL codi	Prope #3931 used c	- 44	#10169	bone m	brain e	י רכ	footal	TIMILLE	Illimine	Secrete	С	Ψ,

ALIGNMENTS

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RESULT 1
AAT96577
                                                                                                                                                         \mbox{Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease; ss.
                                                                                                                                                                                                 22-APR-1998 (first entry)
                                                                                                                                                                                                                 AAT96577;
                                                                                                                                                                                                                                AAT96577 standard; DNA; 583 BP.
                                                                                                                                                                                  Human bcl-w DNA.
                                                                                                                                           Homo sapiens.
      Adams JM, Cory S, Gibson LM, Holmgreen SP;
                                                                                      WO9735971-A1.
                      (AMRA-) AMRAD OPERATIONS PTY LTD.
                                        27-MAR-1996;
                                                      27-MAR-1997;
                                                                     02-OCT-1997.
                                        96AU-0008965.
                                                        97WO-AU00199
                                                                                                                            Location/Qualifiers
                                                                                                     /product= bcl-w
                                                                                                              /*tag=
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1997-489635/45

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RESULT
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                                                                                              541 9999ccctggtaactgtaggggccttttttgctagcaagtgaa 583
                                                                                        541
                                                                                                                                                            481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis,
                                                                                                                                                                                                                                      421 agtgggggctgggcgtgagttcacagctctatacggggacgggggccctggaggaggcgcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's diseases).
                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                          301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody production or screening of potential modulators.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 aagctgaggcagaagggttatgtctgtggagctggccccgggggagggcccagcagctgac
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                                                                           9999ccct9gtaactgtaggggccttttttgctagcaagtgaa 583
                                                                                                                                            cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
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99.5%;
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AAX25134 standard; DNA; 583 BP

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                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other
241 caggtctccgacgaactttttcaagggggccccaactggggccgccttgtagccttcttt 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
                                                                                                                                                                         61 aagctgaggcagaagggttatgtctgtggagctggcccgggggagggcccagcagctgac 120
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                                                                                                             ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc
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               The present sequence is the human bcl-w gene encoding Bcl-w protein (see AAV05530), a pro-survival member of the Bcl-2 family which is converted to the Bcl-2 family which is converted to the provided for spermatogenesis. The invention relates generally to a method of treatment and to an invention relates generally to a method of treatment and to an invention suseful for inducing or reducing fertility of male sequences useful for inducing or reducing fertility of male contains. Methods are provided for the treatment of infertility, or contained and fertility, by modulating spermatogenesis. An animal condel carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for the intertile of 
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                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 32; 52pp; English.
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by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of
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                                                                                                                          ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human
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                                                                                                                                                                                                                     AAV28334 standard; cDNA; 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat
                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttototgatotggoggotoagotgcatgtgaccccaggotcagcccaacaacgottcacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \verb|cogctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc|
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                                                                                                                                                                                                                                                                           ggggccctggtaactgtaggggccttttttgctagcaagtg 581
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                                                                                                                                                                                                                                                                                                                         cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
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                                                                                                                                                                        (first entry)
                                                                              Location/Qualifiers
                                             /product= bcl-y
                                                         /*tag=
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                                  "No stop codon given"
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Pred. No. 3.7e-134;
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04-AUG-1998

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptosic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct expression in vivo. Also, antisense constructs can be used in disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression in vivo. Also, antisense const where prevention of cell death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Column 15/16; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth e.g. cancers
                                                                                                                                                                                                                                                                                      241
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11-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                       | agt99999ct999cg9agttcacagctctatacg9g9acg9g9gccctg9ag9ag9cgcgg 480
9999ccctggtaactgtaggggccttttttgctagcaag 579
                        cgtctgcgggagggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
                                            cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
                                                                                     agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg
                                                                                                                                                gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
                                                                                                                                                                                                                                                                         caggtctccgatgaactttttcaagggggccccaactggggccgccttgtagccttcttt
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                                                                                                                                                                                                                                                                                                                                      ttototgatotggcggctcagctgcatgtgaccccaggctcagcccaacaacgcttcacc
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                                                                                                                                                                                                                                                                                                                                                                                                  ccactgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc
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97US-0798897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 572.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 7.2e-133;
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CC specification also describes rat bel-y protein (Rbcl-y) and the bel-y and the programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y compositions may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be compositions as the cell death inhibitors, they may be composited in the cell death pathway. If they act as cell death inhibitors, they may be composited in the cell sease, neural and muscular degenerative diseases composited the cell muscular degenerative diseases composited the cell death, aging, spinal cord injuries and amyotrophic lateral corditions where cells under go premature cell death as a consult of triggers which may or may not be apparent. They may also be composited period. In contrast, if they act as cell death stimulators, composited cell life span such as cancer (especially kaposi's sarcoma and composited cell life span such as cancer (especially kaposi's sarcoma and conditions cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes human bcl-y protein (Hbcl-y).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW97392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guastella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding the human bcl-y protein.
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97US-0798897.
97US-0978523.
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Matches 575; Conserv

Conservative

98.2%; 99.3%;

Score 572.6; DB 20 Pred. No. 7.2e-133;

DB 20;

Mismatches

Indels Length 579;

0

Gaps

0,

Query Match Best Local

QΥ 밁 Ş 밁 Ş

121

61

aagctgaggcagaagggttatgtctgtggagctggccccgggggagggcccagcagctgac 120

aagctgaggcagaagggttatgtctgtggagctggcccgggggagggcccagcagctgac 120

atggcgaccccagcctcggccccagacacacgggctctggtggaagactttgtaggttat 60 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat

60

61

121

181 ttctotgatotggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc

ccactgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180

ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccaacaacgcttcacc 240

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> 241 241

301

caggtctccgatgaactttttcaagggggccccaactggggccgccttgtagccttcttt 300 caggtotocgacgaactttttoaagggggcoccaactggggcogcottgtagccttcttt 300

181

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ARESULT
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XX SS;
XX SS;
XX SS;
XX Rat
AC CAS
AC C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat bcl-y gene
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11-FEB-1997;
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                                                                   (COCE-) COCENSYS INC
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97US-0798897.
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                                                                                                                                                                                                                                                                                                                                                                                                                         /product= bcl-y
/note= "No stop codon given"
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AAX15945 standard; cDNA; 579

AAX15945;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Column 13/14; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAW61391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression in vivo. Also, antisense const where prevention of cell death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                             481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
                                                                                                                                                                                                         421 agtgggggctggggggggttcacagctctatacgggggacgggggccctggaggaggcgcgg
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                                                             cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggctgtggcactg
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94.5%;
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Pred. No. 9.6
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(first entry)

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The present sequence encodes rat bcl-y protein (Rbcl-y). The C specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and C Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y CC the cell death pathway. If they act as cell death inhibitors, they may be CC used in therapies to treat subjects suffering from: strokes, head trauma, CC (especially multiple sclerosis), myocardial infarction, vitally induced CC (especially multiple sclerosis), myocardial infarction, vitally induced CC cell death, aging, spinal cord injuries and amyotrophic lateral CC used in this way to develop cell lines which remain viable in culture for CC used in this way to develop cell lines which remain viable in culture for CC an extended period. In contrast, if they act as cell death stimulators, CC prolonged cell life span such as cancer (especially kaposi's sarcoma and CC lung cancer) and auto/hyperimmune diseases. They may also be used to xxx
                                                                                                                                                                                                                         Matches 547;
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                     Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Columns 13-16; 26pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; aging; cell death; cell death; cell death; cell death; cell death; cell death; thimulator; prolonged cell life span; kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                          61 aagetgaggcagaagggttatgtetgtggagetggeeeegggggagggeeeageagetgae 120
                                                                                                                                                                                                                                        Local
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11-FEB-1997;
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                                                      aagctgagacagaagggttatgtctgtggagctggccctggggaaggcccagcagccgac 120
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                                                                                                                                                                                                                                90.5%;
                                                                                                                                                                                                           Score 527.8; DB 20;
Pred. No. 9.6e-122;
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The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see AAY()5531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or
                                                                                                                       Claim 3; Page 34; 52pp; English.
                                                                                                                                                            An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                          protein associated with Bcl-w
                                                                                                                                                                                                                  WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                    (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     animal model;
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for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or model carries as mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animal murine bcl-w gene or in a gene associated with bcl-w. Such animally have disorganised seminferous tubules and are substantially have disorganised seminferous tubules and are substantially have disorganised seminferous tubules and are substantially by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;
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                                                        Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
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                                            diagnosis;
                                                                                                                       22-APR-1998
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                                              degenerative disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family. This gene promotes cell survival, so its modulation is useful in family. This gene promotes cell survival, so its modulation is useful in stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, stroke, Alzheimer's disease, myocardial infarct, infection or in cell hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell transplants. Up-regulation of the gene can also be used to modify cell transplants of invivo, e.g. to develop new lines, to facilitate lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w during genetic modification. It can be used to produce recombinant Bcl-w during denetic modification. It can be used to produce recombinant Bcl-w during denetic modification, antibody production or screening of potential modification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams JM, Cory S, Gibson LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p-PSDB; AAW36048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 50-51; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          degenerative diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modulators
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/note= "q"
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91.9%;
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                fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bol'w gene seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including facilitating spermatogenesis in animals, or which can induce include the seminatogenesis in animals, or which can induce
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                                                                                                                        The present sequence is described as a derivative of the mouse bcl-w gene (see AAX25133) and encodes Bcl-w protein (see AAY05533), and which is essential for spermatogenesis. The invention relates identification of molecules and general and to an animal model for the inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mattain in the inventor of the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mattain is a first provided for the treatment of infertility.
                                                                                                                                                                                                                                                                                          Disclosure; Page 38; 52pp; English.
                                                                                                                                                                                                                                                                                                                            protein associated with Bcl-w
                                                                                                                                                                                                                                                                                                                           An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                  Adams J, Cory S, Gibson L,
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Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other:

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  21-JAN-1997;
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                                                                                                                                                                                Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
immunological disorder; autoimmune disease; anti-infectious agent; s
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                          Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                          20-NOV-1998 (first entry)
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                                                                                           /product= "Bcl-like (HAICH29) protein"
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91.9%;
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Pred. No. 2.8e-116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0034204.
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krissansen GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 428.8; DB 19; Length 1098; pred. No. 4.2e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                    Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein gene 120 clone HGBGZ64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thyroid; digestion; osteoporosis; arthritis; testis; lung; thyroid;tis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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07-MAR-1997;
07-MAR-1997;
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                                                                                                                                                                                                                                  11 APR-1997;
23 -MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-1997;
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11-APR-1997;
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                                                                                                                                  23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
                                             23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
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97US-0043569.

97US-0043576.

97US-0043578.

97US-0043580.

97US-004369.

97US-0043670.

97US-0043671.

97US-0043671.
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97US-0047501.
97US-0047502.
97US-0047503.
97US-0047581.
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97US-0040334
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97US-0047585.
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97US-0043314.
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97US-0040626.
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97US-0047593.
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97US-0047615.
97US-0047617.
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97US-0047600
                                                                                      97US-0047601
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19-JAN-1999

conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for described uses).

Sequence 1864 BP; 494 A; 403 C; 506 G; 455 T; 6 other;

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This sequence represents a nucleic acid molecule designated Gene 120 ATCC 209048) which encodes a secreted human protein. The gene can be immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the superior only acid sequences: AAV5951-yamino acid sequences: AAV7951-yamino acid sequences: AA
conditions e.g. by protein or gene therapy. Also, pathological
                                                                                                                                                                                                                                                                                                                New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological
                                                                                                                                                                                                                                                         Claim 1; Page 353-354; 721pp; English.
                                                                                                                                                                                                                                                                                               disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feng Р,
Куаw Н,
                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW74848
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18-AUG-1997
22-AUG-1997
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Lafleur DW, Li Y, Moore PA, N
M, Shi Y, Soppet DR, Young PE,
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97US-0057669.
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970S-0056878
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Yoore PA, Ni J, Olsen HS,
Yn GL, Zeng Z;
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RESULT 13
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02-JUL-2001; 2001WO-EP07537
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                                                                                                                           antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                          WO200200928-A2
                                                                                                              neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                     HOMO sapiens
                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 201.
                                                                                                                                                                                                                                                             26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                 ABL32228 standard; DNA; 6049 BP
                                                                                                                                                                                                                                                                                                                                                                                    431 agtgggggctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 aagotgaggcagaagggttatgtotgtggagotggcocoggggagggcocagcagotgac 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 70
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                                                                                                                                                                                                                                                                                                                                                                                                                             agtgggggctgg 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccaacaacgcttcacc
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99.3%;

    Mismatches

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RESULT 14
ABL3229/c
ID ABL322
XX
AC ABL322
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AC ABL322
XX
DT 26-MAF
XX
DT Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 201; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6049 BP; 1480 A; 109 C; 1549 G; 2911 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases. The present sequence is a gene of the invention.
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                                                           ABL32229
                                                                                        ABL32229 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                               323;
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Similarity 74.68;
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2000DE-1043826.
                               (first entry)
   system
                                                                                          DNA; 6049
   associated gene SEQ ID NO:
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Pred. No. 2.8e-54;
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Query Match
Best Local
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acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular diseases such as retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 202; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6049 BP; 1591 A; 109 C; 1429 G; 2920 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       macular degeneration, arteriosclerosis, anaemia, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1049 ATAACGACCCCAACCTCGACCCCAAACACACGAACTCTAATAACAAACTTTATAAATTAT 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                               698
                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                                                                                                                                                                                                                                                  AAACTAAAACAAAAAATTATATCTATAAAACTAACCCCGAAAAAAACCCCAACAACTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                aagctgaggcagaagggttatgtctgtggagctggcccgggggagggcccagcagctgac 120
                                                                                                                                                                                                                                                                                                                ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
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gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
                                                                                                  caggtotocgacgaactttttoaagggggcoccaactggggcogcottgtagcottottt 300
                                                                                                                                                                          TTCTCTAATCTAACGACTCAACTACATATAACCCCAAACTCAACCCAACAACGCTTCACC
                                                                                                                                                                                                        ttototgatotggoggotoagotgcatgtgacococaggotoagococagocacgottoaco
                                                                                                                                                                                                                                                                                  CCGCTACACCAAACCATACGAACAACTAAAAATAAATTCGAAACCCGCTTCCGACGCACC
                                                                       CAAATCTCCGATAAACTTTTTCAAAAAAACCCCCAACTAAAACCGCCTTATAACCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298;
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                                                                agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                 derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 6077; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from humar breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-496933/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human breast cell single exon nucleic acid probe #6077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to a spatially-addressable set of single exon
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2000US-0608408
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2000US-0234687
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Query Match

25.7%;

Score

150;

DB 22;

Length 150;

Sequence 150 BP; 25 A; 33 C;

65 G;

27 T; 0 other;

from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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                                                       gggaactgggcatcagtgaggacagtgctgacgggggccgtggcactggggccctggta 120
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Search completed: June Job time: 4702 sec 6 2002, 12:02:24

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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seq length: 2000000000
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1: /SIDSI/gogdata/geneseq/geneseqn-embl/NA1990_DAT: *
2: /SIDSI/gogdata/geneseq/geneseqn-embl/NA1990_DAT: *
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTE

Result		Query				
No.	Score	Match Length DB	ength	:	ID	Description
1	577.8	99.3	581	20	AAX25133	Mouse bcl-w gene.
2	563.4	96.8	581	18	AAT96578	Mouse bcl-w DNA.
ω	563.4	96.8	581	20	AAX25135	Mouse bcl-w gene d
4	558.2	95.9	579	19	AAV28333	Rat bcl-y gene. R
v	558.2	95.9	579	20	AAX15945	cDNA encoding the
თ	520.2	89.4	581	20	AAX25132	Human bcl-w gene.
7	519.6	89.3	583	18	AAT96577	Human bcl-w DNA.
8	519.6	89.3	583	20	AAX25134	Human bcl-w gene d
9	515	88.5	579	19	AAV28334	Human bcl-y gene.

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21.6						21.8		•	•	•	22.3	•	•	23.1	23.1	23.1		23.1		23.1	23.1	23.2	25.5	25.5	25.5	25.5	25.5	25.5	25.5	25.5	33.1	37.6	64.0	64.1	88.5
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AAI53868	.03	AAK21876	ABA38761	ABA73433	AAH45295	AAI40812	AAK35096	AAK09207	ABA28894	ABA60917	AAF30926	AAS00250	AAX33182	AAS00247	AAC90810	AAS15189	AAZ93614	AAT40079	AAQ81698	AAH43464	AAH48169	AAF75960	AAI05940	AAI45438	AAI20236	AAK39424	AAK13683	ABA32370	ABA65269	ABA47382	ABL32229	ABL32228	AAV59630	9	AAX15946
Probe #22554 used		Human brain expres	_			e #9498 u	bone marrow	3		toetal		LFn-Bcl-X1 apoptos	Base sequence of t	Bcl-X1-DTR apoptos	Human Bcl-xL nucle	Human bcl-x cDNA.	Bcl-x gene. Homo	Bcl-XL gene. Homo	Human thymus BCL-X	cDNA clone HP03564		Id-type BCI	šed	#14124 used	Probe #10169 for g	Human bone marrow	Human brain expres	Probe #10836 for g			Human immune syste	Human immune syste	Human secreted pro	Nucleotide sequenc	cDNA encoding the

ALIGNMENTS

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An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w $$	WPI; 1999-243890/20. P-PSDB; AAY05531.		Name I Com & Cibeon I Koontgen F. Drint C:	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.		16-SED-1997: 97AU-0009228.		16-GFD-1008. 08WO-AUT00764	25-MAR-1999.		WO9913710-A1.		Mus sp.		animal model; ss.	Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;		Mouse bcl-w gene.		05-JUL-1999 (first entry)		AAX25133;		AAX25133 standard; DNA; 581 BP.	5133	

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RESULT
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 AAT96578
                                  AAT96578 standard;
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579; Conserv
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99.7%;
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Pred. No. 3.4e-145;
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Matches 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                          Sequence 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 50-51; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              degenerative diseases
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P-PSDB; AAW36048.
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570; Conser
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sis; degenerative disease; ss.
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98.1%;
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Pred. No. 2.
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bcl-w gene (see AAX2513), and encodes Bcl-w protein (see AAY2513), pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for identification or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries fertility, by modulating spermatogenesis.
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                                                                                                                                                                                                                                                                                  (HALL-) HALL INST MEDICAL RES
                                                                                                                                                                                                                                                                                                             16-SEP-1997;
                                                                                                                                                 Disclosure; Page 38; 52pp; English.
                                                                                                                                                                          An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                                  P-PSDB; AAY05533
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                                                                                                                      present sequence is described as a derivative of the mouse
                                                                                                                                                                                                                                                            Cory S, Gibson L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no
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                                                                               bc1-2; cell death pathway; apoptotic; apoptosis;
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Pred. No. 2.5e-141;
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             421
              421 agtggcggctgggcggagttcacagctctatacgggggacggggccctggaggaggcacgg 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
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                                                            caagtgcaggattggatggtgacctacctggagacacgcttggctgactggatccacagc
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97US-0798897.
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Pred. No. 6.1
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The present sequence encodes rat bcl-y protein (Rbcl-y). The CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y CC the cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y CC the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, CC (especially multiple sclerosis), myocardial infarction, vitally induced CC (especially my may also be cell death, aging, spinal cord injuries and amyotrophic lateral CC (especially my to develop cell lines which remain viable in culture for CC (especially my to develop cell lines which remain viable in culture for CC (especially may be used to treat conditions associated with CC (especially and bbcl-y may be used to treat conditions associated with concerning and auto/hyperimmune diseases. They may also be used to
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                           cause cell death in, and hence control, parasites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel bcl-y homologues of the rat and human bcl-2 protein for modulating programmed cell death
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11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-214150/18
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Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;

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Best Local Similarity 97.8%;
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                                                                                                                                                                                                                           Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
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               Adams J, Cory S,
                                        (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
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                                                                                                     98WO-AU00764.
                   Gibson L,
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Pred. No. 6.1e-140;
0; Mismatches 13;
                      Koentgen F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the human bcl-w gene encoding Bcl-w protein (see AAY05530), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An animal model exhibiting reduced levels of a Bcl-w protein and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein associated with Bcl-w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other;
                                                                                                                                                                     181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccaggcaacgcttcacc 240
                                                                                                           241
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                                                                                                                                                                                                                                                                                                                                                 aggctgaggcagaagggttatgtctgtggagctggccctgggggaaggcccagccgccgac 120
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gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga
                                                             caggtctccgatgaactttttcaagggggccccaactggggccgccttgtagccttcttt
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93.5%;
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Pred. No. 9.2e-130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
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                                                                                                                                                                                                                                                                                                This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
                                                                                                                                                                                                                                                                           Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
                            121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                            121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 48; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                degenerative diseases
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                                                                                    61 aagetgaggeagaagggttatgtetgtggagetggeeecggggagggeeeageagetgae 120
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diagnosis; degenerative disease; ss.
                                                                                                  61 aggetgaggeagaagggttatgtetgtggagetggeeetggggaaggeeeageegaee 120
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                                                                                                                                           1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
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                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                            543; Conservative
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                                                                                                                                                                                                                       89.3%;
93.3%;
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                                                                                                                                                                                                                    Score 519.6, DB 18 Pred. No. 1.3e-129;
                                                                                                                                                                                                           Mismatches
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         The present sequence is described as a derivative of the human bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries
fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene
                                                                                                                                                                                                An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                     Disclosure; Page 36; 52pp; English.
                                                                                                                                                                                                                                                  P-PSDB; AAY05532
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                                                                                                                                                                                                                                                                                                                                                                                 98WO-AU00764
                                                                                                                                                                                                                                                                                         Gibson L,
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or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 aagetgaggcagaagggttatgtetgtggagetggeeegggggagggeeeagcagetgae 120
                                                                                                                                               02-OCT-1998 (first entry)
                                                                                                                                                                              AAV28334;
                                                                                                                                                                                                        AAV28334 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                      421
                                                                                                                                                                                                                                                                                                                                                                                                                 421 agtggcggctgggcggagttcacagctctatacggggacggggccctggaggaggaggcacgg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 caagtgcaggagtggatggtggcctacctggagacggctggtcgactggatccacagc 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
                                                                                     ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human
                                                                                                                    Human bcl-y gene
                                                                                                                                                                                                                                                                                                                                         481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg
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                                                                                                                                                                                                                                                                               541 ggggccctggtaactgtaggggccttttttgctagcaagtga 582
                                                                                                                                                                                                                                                                                               541 ggggccctggtaactgtaggggccttttttgctagcaagtga 582
                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtgggcattcttt 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543;
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                                                                                                                                                                                                                                                                                                                                                         cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
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                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 519.6; DB 20
Pred. No. 1.3e-129;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct be used to prevent uncontrolled cell growth, either by its direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Column 15/16; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p-PSDB; AAW61392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-446079/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                            121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacacgtttccgccgcacc 180
                                                                                                                                                                      241 caggittccgacgaactittccaagggggccctaactggggccgtcttgtgggcattcttt 300
                                                                                                                                                                                                             181
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                                                                                                                                                            241
    421
           421 agtggcggctgggcggagttcacagctctatacggggacggggccctggaggaggaggcacgg 480
                                                               361 caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc 420
                                                                                                     301 gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
                                                                                                                  301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga
                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                  1 atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
                                                                                                                                                                                                                                                                                                                                                                      1 atggcgaccccagcctcggccccagacacacgggctctggtggaagactttgtaggttat 60
                                                                                                                                                                                                                                                                                                                               ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
                                                                                                                                                                                                                                                                ccactgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc
                                                                                                                                                         caggtctccgatgaactttttcaagggggccccaactgggggccgccttgtagccttcttt
agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                              88.5%;
93.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 515; DB 19;
Pred. No. 2.3e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 579;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Query Match

Local Similarity

Length 579;

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AAX15946
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                       Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced sclerosis conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be an extended period. In contrast, if they act as cell death is timulators, prolonged cell life span such as concer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to
                                                                                                                                                                                                           The present sequence encodes human bcl-y protein (Hbcl-y). The specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: Strokes, head trauma, also homological proteins and proteins are traumants.
                   lung cancer) and auto/hyperimmune diseases. They measure cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Columns 15-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Novel bcl-y homologues of the rat and human bcl-2 protein for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAW97392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COCE-) COCENSYS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX15946 standard; cDNA; 579 BP
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97US-0798897.
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Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

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. 21-JAN-1997;
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                                                              21-JAN-1998;
                                                                                                                                                                                              W09831800-A2.
                                                                                                                                23-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunological disorder; autoimmune disease; anti-infectious agent; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 9999ccct9gtaactgtaggggccttttttgctagcaag 579
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                                                                                                                                                                                                                                    /product= "Bcl-like (HAICH29) protein"
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                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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93.1%;
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Pred. No. 2.3e-128;
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RESULT 3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 12A-12D; 120pp; English.
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                                                              AAV59630 standard; DNA; 1864 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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     (first entry)
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Pred. No. 3.4e-90;
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                      Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic; shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein gene 120 clone HGBGZ64.
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07-MAR-1997;
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23-MAY-1997;
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07-MAR-1997;
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23-MAY-1997;
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f, Shi Y, Sc
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                                                                                                                                             Soppet DR,
                                                                                                                                                  Fischer CL, Flor
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Carter KC, Duan R, Ebner R, Eher CL, Florence KA, Greene JM, Y, Moore PA, Ni J, Olsen HS, DR, Young PE, Yu GL, Zeng Z; Greene JM, Rosen CA; Endress GA;

New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Claim 1; Page 353-354; 721pp; English.

ATCC 209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological sequence represents a nucleic acid molecule designated Gene 120 the human cDNA clone HGBGZ64 (deposited as clone ATCC 97902 and 209048) which encodes a secreted human protein. The gene can be of

02-JUL-2001; 2001WO-EP07537.

03-JAN-2002.

W0200200928-A2 Homo sapiens. neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease

anaemia;

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ABL32228
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                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anae acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                    Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                    26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                      ABL32228;
                                                                                                                                                                                                                                                                                                                                          ABL32228 standard; DNA; 6049 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 agtgggggctgg 442
                                                                                                                                                                                                                                                                                                                                                                                                                                              421 agtggcggctgg 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in the conditions of the polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 caggictocgaigaactttticaagggggccccaactggggccgccitgiagccitcttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (see AAV59511 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ccgctgcaccaagccatgcgggctgctgaggacgagtttgagacccgtttccgccgcacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 aagctgaggcagaagggttatgtctgtggagctggccccgggggagggcccagcagctgac 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 atggcgaccccagcctcggccccagacacgggctctggtggcagactttgtaggttat 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 atggcgaccccagcctcaacccccagacacacgggctctagtggctgactttgtaggctat 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9tctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune system associated gene SEQ ID NO: 201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caggittccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aggotgaggcagaagggttatgtotgtggagotggocotggggaaggcocagcogocogac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccaacaacgcttcacc
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91.2%;
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Best Local
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01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 201; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6049 BP; 1480 A; 109 C; 1549 G; 2911 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5061 aagttgaggtagaagggttatgtttgtggagttggtttcgggggagggtttagtagttgat 5120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5001 atggcgattttagtttcggttttagatatacgggttttggtggtagattttgtaggttat 5060
                                                                                                                                                                                                                        ABL32229 standard; DNA; 6049 BP
                                                                                                                                                                5421 agtgggggttggg 5433
                                                                                                                                                                                                                                                                                                                                                                   241 caggtttccgacgaccttttccaagggggccctaactggggccgtcttgtgggcattcttt 300
Human immune system associated gene SEQ ID NO:
                                                             ABL32229;
                              26-MAR-2002 (first entry)
                                                                                                                                                                                                                                          361 caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 agtggcggctggg 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcgttgtattaagttatgcgggtagttggagatgagttcgagattcgttttcggcgtatt 5180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                                                                                                                     taggttttcgatgaatttttttaagggggttttaattggggtcgttttgtagttttttt 5300
                                                                                                                                                                                                                                                                                                                                                                                                            ttttttgatttggcggtttagttgtatgtgattttaggtttagtttaataacgttttatt 5240
                                                                                                                                                                                                                                                                                                                                                                                                                                        ttototgacotggccgctcagotacacgtgacoccaggctcagcccagcaacgcttcaco 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299;
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2000DE-1043826.
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69.1%;
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Matches 279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 202; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      989
                                                                                                                                                                                                                                                                                                                                                                  121
749 АТСТТТАВАВСТАСАСТАТАТАСТАВАВАТАТСВАСАВАВАВАТАВАВССВСТВАТАВВА
                                                                                                    809 CAAATCTCCGATAAACTTTTTCAAAAAAACCCCAACTAAAACCGCCTTATAACCTTCTTT 750
                                                                                                                                241 caggtttccgacgaacttttccaagggggccctaactgggggccgtcttgtggcattcttt 300
                                                                                                                                                                                                                                               181 ttctctgacctggccgctcagctacacgttgaccccaggctcagcccagcaacgcttcacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                            301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 aggortgaggcagaagggttatgtortgrggagortggcoctggggaaggcoccagcogcogac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-130909/17.
                                                                                                                                                                                                                                                                                                             CCGCTACACCAAACCATACGAACAACTAAAAATAAATTCGAAACCCGCTTCCGACGCACC
                                                                                                                                                                                                                                                                                                                                           ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                 АЛАСТАВАЛСАВАВАВАВТТАТАТСТАТАВАВСТВАСССССВАВЛАВАВАСССАВСАВСТВАС 930
                                                                                                                                                                                                        TTCTCTAATCTAACGACTCAACTACATATAACCCCAAACTCAACCCAACAACGCTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piepenbrock C,
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2000DE-1043826.
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66.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144; Indels
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abnormal
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The invention relates to a spatially-addressable set of single exon CC nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting CC the probes with a collection of detectably labelled nucleic acids CC derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for CC verifying the expression of regions of genomic DNA predicted to CC determining predisposition and/or prognosing breast disease. Gene CC expression analysis is useful for assessing the toxicity of chemical CC diversity of probes for measuring gene expression, with far less bias CC rapid production of functional information from genomic sequence. The cC resent sequence is a single exon nucleic acid probe of the invention. CC printed specification, but was obtained in electronic format directly CC from WIPO at firm wind int/nmh/mmhlished not accument to single extending the cornact of the company of the union int/nmh/mmhlished not accument to single extending the cornact directly considered the contractor of t
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ABA47382
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-023687.

27-SEP-2000; 2000US-0236359.
                    from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; SEQ ID NO 6077; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human breast cell single exon nucleic acid probe #6077.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       629 AAT 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
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Query Match

25.5%; Score 148.4; DB 22; Length 150;

Sequence 150 BP; 25 A; 33 C; 65 G; 27 T; 0 other;

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                                    Qy
                                                                    Вb
                                                                                               γQ
                                                                                                                               В
                                                                                                                                                          δõ
                                                                                                                                                                                      Matches 149; Conserv
121 actgtaggggccttttttgctagcaagtga 150
               553 actgtaggggccttttttgctagcaagtga 582
                                                                    493 999aactgggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctggta 552
                                                                                                                               433 goggagitcacagcictatacggggacggggccctggaggaggaggcacggcgictgcgggag 492
                                                    61 gggaactgggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctggta 120
                                                                                                               1 geggagtteacagetetataeggggaeggggeeetggaggaggegegegtetgeggag 60
                                                                                                                                                                                     149;
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                99.3%;
                                                                                                                                                                                  0;
                                                                                                                                                                              Pred. No. 2.4e-30; 0; Mismatches 1;
                                                                                                                                                                              Indels
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Search completed: June Job time: 4709 sec 6, 2002, 12:02:31

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